

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2006, 00:01:26 ; Search time 820 Seconds
(without alignments)
6504.572 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645

Sequence: 1 GTCAGGTTCAATTCGCTT.....TGTACATGNTAGGCTGC 645

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	645	100.0	1682	7 US-10-389-566-194	Sequence 194, App
2	645	100.0	6550	7 US-10-759-602-1	Sequence 19, App
3	645	100.0	9335	7 US-10-759-602-19	Sequence 8, App
4	557	86.4	709	7 US-10-389-566-8	Sequence 217, App
5	47.6	7.4	1119	7 US-10-389-566-217	Sequence 117, App
6	43.8	6.8	138363	7 US-10-367-094-117	Sequence 17619, A
7	43.4	6.7	130349	8 US-10-741-600-17619	Sequence 23, App
8	42.8	6.6	50000	8 US-10-706-635-23	Sequence 28430, A
9	41.6	6.4	201	8 US-10-741-600-28430	Sequence 866, App
10	40.2	6.2	10710	7 US-10-311-455-866	Sequence 36, App
11	40.2	6.2	33053	7 US-10-433-793-36	Sequence 2045, App
12	40.2	6.2	40862	6 US-10-311-455-2045	Sequence 1, App
13	40.2	6.2	3673778	6 US-10-312-841-1	Sequence 123, App
14	40.2	6.2	3673778	6 US-10-312-841-2	Sequence 123, App
15	39.4	6.1	5376	6 US-10-311-455-2123	Sequence 123, App
16	39.4	6.1	83391	7 US-10-433-793-123	Sequence 4953, App
17	39.2	6.1	6145	8 US-10-723-860-4953	Sequence 215, App
18	39.2	6.1	8757	8 US-10-335-053-215	Sequence 456, App
19	38.8	6.0	7134	6 US-10-311-455-456	Sequence 328, App
20	38.8	6.0	10467	6 US-10-240-453-328	Sequence 520090, App
21	38.6	6.0	602	4 US-09-925-065A-520090	Sequence 490, App
22	38.6	6.0	5930	6 US-10-311-455-490	Sequence 78, App
23	38.6	6.0	7108	7 US-10-257-166-78	

24	38.6	6.0	9905	6 US-10-311-455-35	Sequence 35, App
25	38.6	6.0	10329	6 US-10-311-455-2095	Sequence 2095, App
26	38.6	6.0	10886	6 US-10-311-455-2107	Sequence 254, App
27	38.6	6.0	13511	6 US-10-311-455-254	Sequence 950, App
28	38.6	6.0	18512	6 US-10-311-455-950	Sequence 956249, App
29	38.4	6.0	581	4 US-09-925-065A-956249	Sequence 2, App
30	38.4	6.0	581	4 US-09-925-065A-956249	Sequence 2, App
31	38.4	6.0	3673778	6 US-10-312-841-2	Sequence 213023, App
32	38.2	5.9	599	5 US-10-027-632-213023	Sequence 193, App
33	38.2	5.9	599	6 US-10-027-632-213023	Sequence 24005, A
34	38.2	5.9	9707	6 US-10-311-455-1393	Sequence 513811, App
35	37.8	5.9	624	7 US-10-424-599-24005	Sequence 513812, App
36	37.6	5.8	595	4 US-09-925-065A-513811	Sequence 623543, App
37	37.6	5.8	595	4 US-09-925-065A-513812	Sequence 551050, App
38	37.6	5.8	634	4 US-09-925-065A-513810	Sequence 551051, App
39	37.6	5.8	658	4 US-09-925-065A-623543	Sequence 551052, App
40	37.6	5.8	1076	4 US-09-925-065A-551050	Sequence 551052, App
41	37.6	5.8	1076	4 US-09-925-065A-551051	Sequence 551052, App
42	37.6	5.8	1076	4 US-09-925-065A-551052	Sequence 1, App
43	37.6	5.8	38596	3 US-09-960-870-1	Sequence 1, App
44	37.6	5.8	38596	3 US-09-960-858-1	Sequence 1, App
45	37.6	5.8	38596	7 US-10-251-668-1	Sequence 1, App

ALIGNMENTS

RESULT 1
US-10-389-566-194
; Sequence 194, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52990)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194
; LENGTH: 1682
; TYPE: DNA
; ORGANISM: Zea mays
US-10-389-566-194
Query Match 100.0%; Score 645; DB 7; Length 1682;
Best Local Similarity 100.0%; Pred. No. 2.8e-164;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCAGGTTCAATTCGCTTCTCTGTATGTTCTTTATTTACAGCTTGACAAAGCT 60
319 GTCAGGTTCAATTCGCTTCTCTGTATGTTCTTTATTTACAGCTTGACAAAGCT 378
DB 1 GTCAGGTTCAATTCGCTTCTCTGTATGTTCTTTATTTACAGCTTGACAAAGCT 378
QY 61 ATAAAGTTGATCTGAGATATATTAACAAGTTGACGACAAAGTTTGATCTTCAAG 120
379 ATAAAGTTGATCTGAGATATATTAACAAGTTGACGACAAAGTTTGATCTTCAAG 438
DB 121 TCTTTAATATATGTTGGTGCATTAATTAAGATTAATCAATTAAGAGTTTGCAAG 180
439 TCTTTAATATATGTTGGTGCATTAATTAAGATTAATCAATTAAGAGTTTGCAAG 498
QY 181 AGAAGTGAAGGCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 240
DB 499 AGAAGTGAAGGCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 558
QY 241 AATACTGAATGACCTTGCTAGCATGCTTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 300

Db 559 AATAACTGAATGACCTGTGTGCTACAGCCCAATGATTTAGAAAGGTAGATGGGAA 618

Qy 301 ATCTAATATTAATTTGGCTAATCTTTAGTACTAATTAATGATGATGAAAGCCTACAAAT 360

Db 619 ATCTATATATTAATTTGGCTAATCTTTAGTACTAATTAATGATGATGAAAGCCTACAAAT 678

Qy 361 GCCCATGCAGGCCCTAATGTCCCGGTGACATGATTTAGCGCAGTACTATGATTAATTAATCT 420

Db 679 GCCCATGCAGGCCCTAATGTCCCGGTGACATGATTTAGCGCAGTACTATGATTAATTAATCT 738

Qy 421 CTATTGTTCTCCTTTTGTAGTGTCTGATPAAGATGCTTTTGTGAGCCACTCGAAG 480

Db 739 CTATTGTTCTCCTTTTGTAGTGTCTGATPAAGATGCTTTTGTGAGCCACTCGAAG 798

Qy 481 ATGTTTACTTAATCTAGTGGCGAATGATTTGAGGCTCTAGTGCACAGCATGTGCTGT 540

Db 799 ATGTTTACTTAATCTAGTGGCGAATGATTTGAGGCTCTAGTGCACAGCATGTGCTGT 858

Qy 541 AATCTACTGTCAACAATACTCTGTAGTGTGTGCTTAAACTCTAAACTATTTCCAGTGGCT 600

Db 859 AATCTACTGTCAACAATACTCTGTAGTGTGTGCTTAAACTCTAAACTATTTCCAGTGGCT 918

Qy 601 AGTAATTAACCAATCAATTAACAACAATGTTACATGTGTGAGGGCTGC 645

Db 919 AGTAATTAACCAATCAATTAACAACAATGTTACATGTGTGAGGGCTGC 963

RESULT 2
US-10-759-602-1

GENERAL INFORMATION:
APPLICANT: Ainley, Michael

Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Paredddy, Dayakar
Pecolino, Joseph F.
Smith, Kelley
Woosley, Aaron

TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: DowAgroSciences LLC
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/759,602
FILING DATE: 16-Jan-2004
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 5110
TELEFAX: 317 337 4847
SEQUENCE DESCRIPTION: SEQ ID NO: 1

US-10-759-602-1

Query Match	100.0%;	Score 645;	DB 7;	Length 6550;
Best Local Similarity	100.0%;	Pred. NO. 5.3e-164;		
Matches 645; Conservative	0;	Mismatches	0;	Gaps 0;

1 GTCAGGTTCAATTCGCTTCCCTGTATGTTCTTATATTAACATGCTCTGACAAAGCT 60
 |||||
 |||||

Db	4420	GTCAAGGTCAATCTCTCTCCCTGTTATGTTCTTATATTTACATGCTCTGCACAAAGCT	44479
Qy	61	ATTAAAGCTGTATCTGAGATTAATAATAAAGTACTCTACAAAGTTTGATCTAAAG	120
Db	4480	ATTAAAGCTTATATCTGAGATTAATAATAAAGTACTCTACAAAGTTTGATCTTAAG	4539
Qy	121	TCTTTTAATAATAGTTGGTGCAATAGATTATGAGTAATCCATATAAAGGTGTTCAG	180
Db	4540	TCTTTTAATAATAGTTGGTGCAATAGATTATGAGTAATCCATATAAAGGTGTTCAG	4599
Qy	181	AGAAATGAAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTATCAAGC	240
Db	4600	AGAAATGAAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTATCAAGC	4659
Qy	241	AATACCTGAAAGCACTGTGCTAGATGATGCTTAAGTATAGAAAGGTGATGGGAGA	300
Db	4660	AATACCTGAAAGCACTGTGCTAGATGATGCTTAAGTATAGAAAGGTGATGGGAGA	4719
Qy	301	ATCATATATATTTTGGCTAACTTCTTATAGTATCTATGATGATGAGAAAGCCATCAAT	360
Db	4720	ATCATATATATTTTGGCTAACTTCTTATAGTATCTATGATGATGAGAAAGCCATCAAT	4779
Qy	361	GCCCATGCGAGCCCTTAATGTCGCCGTGACATGATGAGCCAGTACTATGATTAATTTACT	420
Db	4780	GCCCATGCGAGCCCTTAATGTCGCCGTGACATGATGAGCCAGTACTATGATTAATTTACT	4839
Qy	421	CTATGTGTCCTTTTGTAGTGCTGTATAGATGATGCTTTTGTAGCCCTGAGAG	480
Db	4840	CTATGTGTCCTTTTGTAGTGCTGTATAGATGATGCTTTTGTAGCCCTGAGAG	4899
Qy	481	ATGTTTACTTAATCTATAGTGGCAATGATGAGACTCTAGTGCAAGCATGTGCTGT	540
Db	4900	ATGTTTACTTAATCTATAGTGGCAATGATGAGACTCTAGTGCAAGCATGTGCTGT	4959
Qy	541	AATCTACTGTACCACTACTCTGTAGTGTGTCTTAAACTTAAACTTATTCAGAGTGCT	600
Db	4960	AATCTACTGTACCACTACTCTGTAGTGTGTCTTAAACTTAAACTTATTCAGAGTGCT	5019
Qy	601	AGTAATTAACCAATGATTTACAAACCTGTATCAATGTAAGGGCTGC	645
Db	5020	AGTAATTAACCAATGATTTACAAACCTGTATCAATGTAAGGGCTGC	5064

RESULT 3
US-10-75

US-10-759-602-19
; Sequence 19, Application US/10759602
; Publication No. US20040143868A1

GENERAL INFORMATION:

APPLICANT: Ainsley, Michael
 Armstrong, Katherine
 Belmar, Scott
 Folkerets, Otto
 Hopkins, Nicole
 Menke, Michael A.
 Paraddy, Dayakar
 Petolino, Joseph F.
 Smith, Kelley
 Woosley, Aaron
 TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DowAgroSciences LLC
 STREET: 9330 Zionsville Road
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: USA

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;      COMPUTER READABLE FORM:
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;      MEDIUM TYPE: Floppy disk
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;      COMPUTER: IBM PC compatible
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;      OPERATING SYSTEM: PC-DOS/MS-DOS
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;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;      CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/10/759,602
/ FILING DATE: 16-Jan-2004
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Kraus, Eric J
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 317 337 5110
/   TELEFAX: 317 337 4847
/ INFORMATION FOR SEQ ID NO: 19:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 935 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: double
/     TOPOLOGY: circular
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-759-602-19

Query Match      100.0%; Score 645; DB 7; Length 935;
Best Local Similarity 100.0%; Pred. No. 6,3e-164;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAGGTTCAATTCGCTTCTCTGTATGTTCTTTATATTAATGCTCTGCAAAAGCT 60
DB 1758 GTCAGGTTCAATTCGCTTCTCTGTATGTTCTTTATATTAATGCTCTGCAAAAGCT 1817
QY 61 ATTTAAAGCTTGATCTGCAATTAATTAACAAGTTCACAAAGTTTGTACTTCAAG 120
DB 1818 ATTTAAAGCTTGATCTGCAATTAATTAACAAGTTCACAAAGTTTGTACTTCAAG 1877
QY 121 TCTTTTAACTATATGTTGGTGCAATTAAGATTATGAGTAATCCATATGAAGGTGCAAG 180
DB 1878 TCTTTTAACTATATGTTGGTGCAATTAAGATTATGAGTAATCCATATGAAGGTGCAAG 1937
QY 181 AGAACAAGAAAGCAAAAGATTAACGAGATGAACCCATTACTAGCTTTGGCTGATCAGACC 240
DB 1938 AGAACAAGAAAGCAAAAGATTAACGAGATGAACCCATTACTAGCTTTGGCTGATCAGACC 1997
QY 241 AATTAATTTGAATGCACTTGCTGACATGCTTAAGTATTAAGAAAGTATGATGGAGAA 300
DB 1998 AATTAATTTGAATGCACTTGCTGACATGCTTAAGTATTAAGAAAGTATGATGGAGAA 2057
QY 301 ATCTATATATTTTGGCTAATCTCTTAACTTACTTATTTGATGAGAAAGCTTACCAAT 360
DB 2058 ATCTATATATTTTGGCTAATCTCTTAACTTACTTATTTGATGAGAAAGCTTACCAAT 2117
QY 361 GCCCATGCAAGCCCTAATGTCCTGGGTGACATGATGAGCCAGTACTATTAATTACT 420
DB 2118 GCCCATGCAAGCCCTAATGTCCTGGGTGACATGATGAGCCAGTACTATTAATTACT 2177
QY 421 CTAATGTTCTCTTTTGAAGTCTGTATTAAGTGTCTTTTGAAGCACTCGAAG 480
DB 2178 CTAATGTTCTCTTTTGAAGTCTGTATTAAGTGTCTTTTGAAGCACTCGAAG 2237
QY 481 ATGTTTACTTAACTCTAGTGGCAATGATGAGGCTCTGAGTCAAGCGATGCTCTGT 540
DB 2238 ATGTTTACTTAACTCTAGTGGCAATGATGAGGCTCTGAGTCAAGCGATGCTCTGT 2297
QY 541 AATCTAAGTCAACCACTACTCTGTAGTGTGTGCTTAACTTAACTTATTCACGTGGCT 600
DB 2298 AATCTAAGTCAACCACTACTCTGTAGTGTGTGCTTAACTTATTCACGTGGCT 2357
QY 601 AGTAATTAACCAATCAATTTACACACATGTTTACATGTGTAGGGCTGC 645
DB 2358 AGTAATTAACCAATCAATTTACACACATGTTTACATGTGTAGGGCTGC 2402

RESULT 4
US-10-389-566-8
/ Sequence 8; Application US/10389566
/ Publication No. US20040025202A1
/ GENERAL INFORMATION:
/ APPLICANT: Monsanto Technology, LLC
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/ APPLICANT: Laurie, Cathy C
/ TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
/ FILE REFERENCE: 38-77(52900)D
/ CURRENT APPLICATION NUMBER: US/10/389,566
/ PRIOR FILING DATE: 2003-03-31
/ PRIOR APPLICATION NUMBER: US 60/365,301
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/391,786
/ PRIOR FILING DATE: 2002-06-25
/ PRIOR APPLICATION NUMBER: US 60/392,018
/ PRIOR FILING DATE: 2002-06-26
/ NUMBER OF SEQ ID NOS: 2459
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 709
/ TYPE: DNA
/ ORGANISM: Zea mays
US-10-389-566-8

Query Match      86.4%; Score 557; DB 7; Length 709;
Best Local Similarity 99.1%; Pred. No. 1.4e-140;
Matches 560; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 81 ATATATTAACAAGTTAGCTACACAAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGT 140
DB 1 ACAATATTAACAAGTTAGCTACACAAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGT 60
QY 141 GCAATTAAGTTATGAGTAATCCATATGAAGTGTGTCAGAGAAACAAAGCAAGAT 200
DB 61 GCAATTAAGTTATGAGTAATCCATATGAAGTGTGTCAGAGAAACAAAGCAAGAT 120
QY 201 AAACGATGAACCCATTACTAGCTTTGGCTGTATGACCAATTAATCTTGAATGCACTTG 260
DB 121 AAACGATGAACCCATTACTAGCTTTGGCTGTATGACCAATTAATCTTGAATGCACTTG 180
QY 261 TGTACATAGCTCCTAATGATTTAGAAAGTAGCATGGAGAAATCTATATTTTGGCTAA 320
DB 181 TGTACATAGCTCCTAATGATTTAGAAAGTAGCATGGAGAAATCTATATTTTGGCTAA 240
QY 321 CTTCTTTAGTTACTATTTGATGATGAGAAAGCCCTACATTTGCCATGCAAGCCCTAATGT 380
DB 241 CTTCTTTAGTTACTATTTGATGATGAGAAAGCCCTACATTTGCCATGCAAGCCCTAATGT 300
QY 381 CCGGTGACATGATTTGAGGCAAGTACTATTAATTTACTTATTTCTCTTTTGA 440
DB 301 CCGGTGACATGATTTGAGGCAAGTACTATTAATTTACTTATTTCTCTTTTGA 360
QY 441 GTGCTGTATTAAGTGTCTTTTGAAGCACTCGAAGAGATGTTTACTTAACTTAACTAGTG 500
DB 361 GTGCTGTATTAAGTGTCTTTTGAAGCACTCGAAGAGATGTTTACTTAACTTAACTAGTG 420
QY 501 CGCAATGATTTGAGGCTCTGAGTGCAACGATGTCTGTAACTAATCTGACCACTACT 560
DB 421 CGCAATGATTTGAGGCTCTGAGTGCAACGATGTCTGTAACTAATCTGACCACTACT 480
QY 561 CTGTAGTGTGTCTTAACTCTTAACTTATTTCCAGTGTAGTAACTTAACTAATTTTAC 620
DB 481 CTGTAGTGTGTCTTAACTCTTAACTTATTTCCAGTGTAGTAACTTAACTAATTTTAC 540
QY 621 AACACTGTATACATGTTAGGGCTGC 645
DB 541 AACACTGTATACATGTTAGGGCTGC 565

RESULT 5
US-10-389-566-217
/ Sequence 217; Application US/10389566
/ Publication No. US20040025202A1
/ GENERAL INFORMATION:
/ APPLICANT: Monsanto Technology, LLC
/ APPLICANT: Laurie, Cathy C
/ TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
/ FILE REFERENCE: 38-77(52900)D
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/ CURRENT APPLICATION NUMBER: US/10/389,566
/ CURRENT FILING DATE: 2003-03-31
/ PRIOR APPLICATION NUMBER: US 60/365,301
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/391,786
/ PRIOR FILING DATE: 2002-06-25
/ PRIOR APPLICATION NUMBER: US 60/392,018
/ PRIOR FILING DATE: 2002-06-26
/ NUMBER OF SEQ ID NOS: 2459
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 217
/ LENGTH: 1119
/ TYPE: DNA
/ ORGANISM: Zea mays
US-10-389-566-217

Query Match
Best Local Similarity 7.4%; Score 47.6; DB 7; Length 1119;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 584 AACTATTCACGCGGTAGTAATTAATCCATCATTTACAAACAGCTGTTAGAGGCT 643
DB 15 AACAGGTAGCGACACAGTAATTAATCCATCATTTACAAACAGCTGTTAGAGGCT 74
QY 644 GC 645
DB 75 GC 76

RESULT 6
US-10-367-094-117/c
/ Sequence 117, Application US/10367094
/ Publication No. US20040170982A1
/ GENERAL INFORMATION:
/ APPLICANT: David W. Morris
/ APPLICANT: Marc Malandro
/ TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
/ FILE REFERENCE: 529452001500
/ CURRENT APPLICATION NUMBER: US/10/367,094
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 203
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 117
/ LENGTH: 138363
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(138363)
/ OTHER INFORMATION: n = A,T,C or G
US-10-367-094-117

Query Match
Best Local Similarity 6.8%; Score 43.8; DB 7; Length 138363;
Matches 93; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 37 TATATTACATGCTCTGACAAAGCTATAAGCTGATAGCTGATATATATTAACAAGTTA 96
DB 68785 TCTTTGACTGCTGCTAGGAAGGCACTGACATTTATTAAGTGTGTTACTATATCCATTA 68726
QY 97 GCTACACAAAGTTTGTACTCAAGCTCTTTAATCTATATATGTTGGTGCATTAAGATTATGAG 156
DB 68725 ACTTCATCAGTAAGAGTACTCAAAATTAATCTGATGTAATCCCTTAACAAATTTCTGTGATGG 68666
QY 157 TAATCCATATGAAGGTGTGCAAGACATGAAGCAAGCAAGATTAACGATGA 211
DB 68665 TATATATATATGCTTGTGTTTCAACGAAGATTAATGCGATGTTAAACAGTTCA 68611

RESULT 7
US-10-741-600-17619/c
/ Sequence 17619, Application US/10741600
/ Publication No. US20050026169A1
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```
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001499
/ CURRENT APPLICATION NUMBER: US/10/741,600
/ CURRENT FILING DATE: 2003-12-22
/ NUMBER OF SEQ ID NOS: 73997
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17619
/ LENGTH: 130349
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-741-600-17619

Query Match
Best Local Similarity 6.7%; Score 43.4; DB 8; Length 130349;
Matches 92; Conservative 1; Mismatches 82; Indels 0; Gaps 0;

QY 37 TATATTACATGCTCTGACAAAGCTATAAGCTGATAGCTGATATATATTAACAAGTTA 96
DB 64786 TCTTTGACTGCTGCTAGGAAGGACTGACCATTTATTTAAGTGTCTACTATATCAATTA 64727
QY 97 GCTACAAAGTTTGTACTTCAAGTCTTTTAATATATGTTGGCAATPAAGTTATGAG 156
DB 64726 ACTTCATCAKTAAGAGTACTCAAAATTAATCTTGATGTACCTTAACAAATTTCTGTGATGG 64667
QY 157 TAATCATATGAAGGTGTGCAAGACATGAAGCAAGCAAGATTAACGATGA 211
DB 64666 TATATATATATGCTTGTGTTTCAACGAGATTAATATGAGATTGTTAAACAGTTCA 64612

RESULT 8
US-10-706-635-23/c
/ Sequence 23, Application US/10706635
/ Publication No. US20050014263A1
/ GENERAL INFORMATION:
/ APPLICANT: Meyer, Richard W.
/ APPLICANT: Li, Yi
/ TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
/ TITLE OF INVENTION: Vertebrate Cells
/ FILE REFERENCE: UF-221C1X21
/ CURRENT APPLICATION NUMBER: US/10/706,635
/ CURRENT FILING DATE: 2003-11-12
/ PRIOR APPLICATION NUMBER: 09/086,651
/ PRIOR FILING DATE: 1998-05-29
/ PRIOR APPLICATION NUMBER: 09/662,254
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: 60/224,479
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 23
/ LENGTH: 50000
/ TYPE: DNA
/ ORGANISM: Ambacta moorei entomopoxvirus
US-10-706-635-23

Query Match
Best Local Similarity 6.6%; Score 42.8; DB 8; Length 50000;
Matches 146; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 27 TTATGTTCTTATATATACATGCTCTGACAAAGCTATAAGCTGATAGCTGATATATATA 86
DB 11134 TGATATTAATGTAATATATATATATATTTCTATTAAGTATTAATATTAAGATATATA 11075
QY 87 TAAAGATTAGTACAAAGTTTGTACTTCAAGTCTTTTAATATATGTTGGTGCAATA 146
DB 11074 TAATTAATPAAGAAACAGATTTTACTGTAATATATTTTAATTTTACAAAAGTATATC 11015
QY 147 AGATTATGATATCCATATGAAGGTGTGCAAGACATGAAGCAAGCAAGATTAACGG 206
DB 11014 TTATTAATCGCATGTTTGCAACACAGATTGAAGAAAATATCAAAATATATATATATATAGT 10955
```

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Oy      207  TTGAACCCATTACTGTCCTTGGCTGTATCAGACCAATACTGGAATGCACTTGGCTAG 266
Db      10954 AAATTTAAATTTTGGATTTCTTTGATGCTTTAATTAATTAAGAAATATATTATAGCA 10895
Oy      267  CATGCTTAAGTATTAGAAAAGGTAGCATGGAGAAATCTATATTATTTTGGCTAACTTCT 326
Db      10894 CAATACAGTAATTAATTAATTAACGTATTATTAAATTAATTAATGTTATATATACAAA 10835
Oy      327  TAGTACTATTGATTGAT 344
Db      10834 AAGTTATTATATTTTCAT 10817

RESULT 9
US-10-741-600-28430/c
; Sequence 28430, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28430
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-28430

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Query March 5.4%: Score 41.6; DB 8; Length 201.
Best Local Similarity 52.4%: Pred. No. 0.63;
Matches 89; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

Qy 37 TATATTACATGCTCTGCAGCAAAAGCTATAAAGCTTATACCTGCAGATATATATTAACAATTAA 96
Db 170 TCTGTACTCTCTGTAGGAAGGCACTGACATTTATTTAACTGCTTACTATATTCATTA 111
Qy 97 GCTACACAAGTTTGTACTTTCAGTCTTTTAACTATATATGTTGTGCATTAAGATTATGAG 156
Db 110 ACTTCATCAKTAAGAGTACTCAAAATATCTTGATGACCTTAACAATAATTTCTGTATGG 51
Qy 157 TAATTCATATGAAGTGTGCAAGAAACATGAAGAAGCAAAATGAATTAACGG 206
Db 50 TATTATATATGCTTGTGTTTTTCAACGAAGATAATGCAATGTTTAAACAG 1

RESULT 10
US-10-311-455-866
Sequence 866, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of diseases Associated with the Immune System by Detect
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 866
LENGTH: 10710
TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-866

Query Match
Best Local Similarity 50.3%; Pred. No. 11;
Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTTCAATTCGCTTCCTCTGTTATGTTCTTTATATTAACATGCTCGACAAAGCTATA 63
DB 10207 AAAGTTGAAATVGGAATTTTTTTTTTTATATTTATATTAATAAATTTAATTTAAGATGATTAA 102666

QY 64 AAGCTTATATCTGCAGTATATATTAACAAGTTAGCTACCAAGTTTGTACTTCAAGTCT 123
DB 10267 AGATTTTAAATGTTAAGATTTTAAATTTTAAAAATTTTAAAGAAAATTTTAAAGTTATATTAT 10326

QY 124 TTATACATATATGTTGGCAATTAAGATTATGAGTAATTCATATGAAAGGTGTGCAAGAGA 183
DB 10327 TTAGAGATATAGGTAACGGGTATAGGATTTTATATTTAAATATTTAAAGTAAATGTAATATAA 10386

QY 184 ACATGAAAGCCAAAGAT 200
DB 10387 AGTTAAATAATGATTAAT 10403

RESULT 11
US-10-433-793-36
; Sequence 36, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/433,793
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 212
; SEQ ID NO 36
; LENGTH: 33053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-433-793-36

Query Match
Best Local Similarity 50.3%; Pred. No. 20;
Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTTCAATTCGCTTCCTCTGTTATGTTCTTTATATTAACATGCTCGACAAAGCTATA 63
DB 6176 AAAGTTGAAATVGGAATTTTTTTTTTTATATTTATATTAATAAATTTTAAAGATGATTAA 6235

QY 64 AAGCTTATATCTGCAGTATATATTAACAAGTTAGCTACCAAGTTTGTACTTCAAGTCT 123
DB 6236 AGATTTTAAATGTTAAGATTTTAAATTTTAAAAATTTTGAAGAAAATTTAGTAAATATTAT 6295

QY 124 TTATACATATATGTTGGCAATTAAGATTATGAGTAATTCATATGAAAGGTGTGCAAGAGA 183
DB 6296 TTAGAGATATAGGTAACGGGTATAGGATTTTATATTTAAATATTTAAAGTAAATGTAATATAA 6355

QY 184 ACATGAAAGCCAAAGAT 200
DB 6356 AGTTAAATAATGATTAAT 6372

RESULT 12
US-10-311-455-2045
; Sequence 2045, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian

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: APPLICANT: BERLIN, Kurt
: TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
: TITLE OF INVENTION: cyclosporine methylation
: FILE REFERENCE: 5013.1014
: CURRENT APPLICATION NUMBER: US/10/311,455
: CURRENT FILING DATE: 2002-12-16
: PRIOR APPLICATION NUMBER: PCT/EP01/07537
: PRIOR FILING DATE: 2001-07-02
: PRIOR APPLICATION NUMBER: DE 10032529.7
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: DE 10043826.1
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 2424
: SEQ ID NO 2045
: LENGTH: 40862
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: US-10-311-455-2045

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Query Match	6.2%	DB	6	Length	40862
Similarity	Pred. No. 22				
Best Local	50.3%				
Matches	99	Mismatches	98	Indels	0
				Gaps	0

QY 4 AAGGTCGAATTCGCTTCCCTGCTTAACTCTTAAATTAACATGCTCGAATAAAGCTATA 63
Db 22502 AAGGTGGAATTCGATTTTTTTTTTAATAATTAATAAAAAATTAAATTAAGTGGATTA 22561

QY	64	AACTGTGATCTCGAGTAAATTAACAAGTAGCTACACAAAGTTTGTACTTCAAGCT	123
Db	22562	AGATTTAACGTTAGATTAAAAATTATAAAAATTTTGAAGAAAAATTTAGGATTATAT	22621

QY	124	TTTTACTATATGTTGGTCGACATTAAGATTATAGATTAATCCATATGAAAGGTGTTCCAAAGA	183
Db	22622	TTTGGATTATAGGTATATGGGTAAAGATTATATGTTTAAATATTTAAAGTAATGGTATTTAA	22661

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Oy      184 ACATGAAGCCAAGAT 200
          |||||
Db      22682 AGATAAATTCATAAT 22698

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RESULT 13
US-10-312-841-1
: Sequence 1, Application US/10312841

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; Publication NO. US2003018627/A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Epigenomics AG
;
; TITLE OF INVENTION: Diagnose von b

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; FILEREFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2

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; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence

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! FEATURE:
! OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
! FEATURE:
! NAME/KEY: measure
!

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US-10-312-841-1
LOCATION: (3294164)
; Query Match

Best Local Similarity	50.3%	Pred. No. 1.8e+02	
Matches	99	Mismatches	98
		Indels	0
		Gaps	0

QY	4	63
AAAGTTCATCTCGCTTCTCTGTATGTTCTTAAATTACATGCTCTGACAAAGCTATA		
722859	AAAGTGAATAGGATTTTTTTTTTATTTATATAAAAAATTAATTTAGTGGATTTAA	722918

Db 722859 AAAGTTGAATAAGATTCTTTTCTTATACTTTATATAAAATTAATTTAAGATGATTAA 722

Qy 64 AAGCTTGATACGACGATATAATAACAAGTTAGCTACACAAGTTTGTACTTCAAGTCT 123

Accession	Sequence	Position
D6	AGAAATTAAATGTTAGATTAAATAATTAATAAAATTTTACGAGAAAATTAGTAATATTAT	722978
D6	722919	
D6	TTTAACTATATGTTGTGTCCAATTAAGATTATAGTAATTCATATGAAAGGTTCGAAGA	183
D6	722979	
D6	TTAGAGATTAGTGTGGTAAAGAAATTTATGATTTAAATTTAAAAAGTAAACGTAATAAA	723038
D6	184	
D6	ACATGAAGGCAAGAT	200
D6	723039	
D6	AGTTAAATTAGATAAT	723055

RESULT 14
US-10-312-841-2
; Sequence 2, Application US/10312841

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; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose v

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; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2

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; SEQ ID NO 2
;
; LENGTH: 3673778
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;

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```
;
; FEATURE: chemically created genomic DNA (Homo sapiens)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: unsure
;
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! LOCATION: (3/5015)
US-10-312-841-2
Query Match

4	AGGTCATTCCTGCTCTGTATGTTTATATATACATGCTCTGACAAAGCTATA	63
Rest Local Similarity	4.8%	Ident. No. 4.0e+02
Matches 117;	Conservative	Mismatches 128;
		Indels 0;
		Gaps 0.

DB	404163	AAGAAAGAAATGGATTTTATTTTATTTATATATATATTTAAAGATACATTTAA	4042222
OV	64	AGCTTGATACGAGTATATATATACAGATTAGCTACACAAGTTTGTACTTCAGTCT	123

Db 404223 AGATTAAATGTATAATTTCGAAATTATAAATTTGTAGAGAAAAATATAGAAAAAGTTT 404282

Db 404283 TTAGGAAATAAGTTTAGGTAAAGATTTTATGATTAAAGATTTTAAAGATATTAGTAATAAA 404342

Db 404343 ATTAATAATCGATAATGATTTATTAATTAATAAAGCTTTTCGTATAGTAAAAAGAAAT 404402

Db 404403 AATT 404407

RESULT 15
US-10-311-455-2123
; Sequence 2123, Application US/10311455
Publ: 201401230001
US/10311455-2123

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; GENERAL INFORMATION:
;; APPLICANT: OLEK, Alexander
;; APPLICANT: PIEPENBROCK, Christian
```

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; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; TITLE OR INVENTION: Cytosine Methylation
; FILE REFERENCE: 5013.1014

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; CURRENT APPLICATION NUMBER: US/10/311,45
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537

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/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 2123
/ LENGTH: 5376
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)
US-10-311-455-2123

Query Match 6.1%; Score 39.4; DB 6; Length 5376;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 118; Conservative 0; Mismatches 131; Indels 0; Gaps 0;
QY 4 AAGGTCGAATTCGCTTCTGTTAGTCTTTATATTACATGCTGACAAAGCTAT 63
DB 1188 AAAATTGAATTGGATTTTATTATTATATATAAAATTAAATTAGATGATTA 1247
QY 64 AAGCTTGATACGTCAGTATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAGCT 123
DB 1248 AGATTTAAATGTAAATTTTAAATTTTAAAGTAAATTTAGAGTAAATTTAT 1307
QY 124 TTTACTATATGTGTGTCATATAGATATGATATCCATATGAAGGTGTCAGAGA 183
DB 1308 TTGAATATATAGTAGAGATTAAGATTTTGAAGAAGATGTAAAGTAAATGTGATAA 1367
QY 184 ACATGAAGGCAAGATTAACGATGAACCATTAAGCTTGGCTGATCAGACCAAT 243
DB 1368 AGAAAAAATTAAATTAATGATATTAAATTAATTAAGAGTTTGTATTAGTAAATTAAT 1427
QY 244 AACTTGAAA 252
DB 1428 TATTATATA 1436

Search completed: February 12, 2006, 00:19:58
Job time : 831 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:58:37 ; Search time 179 Seconds
(without alignments)
6405.180 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645
Sequence: 1 GTCAAGTTCATCTGCTT.....TGTTCATGTAGGCGTCG 645

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued Patents NA:*
2: /cgn2_6/prodata/1/ina/1 COMB.seq:*
3: /cgn2_6/prodata/1/ina/5 COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	645	100.0	6550	3	US-09-097-319A-1
2	645	100.0	6550	3	US-09-643-971-1
3	645	100.0	9335	3	US-09-097-319A-19
4	645	100.0	9335	3	US-09-643-971-19
5	43.8	6.8	83178	3	US-09-949-016-14606
6	43.4	6.7	601	3	US-09-949-016-103411
7	42.8	6.6	50000	3	US-09-662-254B-23
8	40.8	6.3	1055	3	US-09-806-708B-23
9	40.2	6.2	1141	3	US-09-806-708B-22
10	39.6	6.1	124480	3	US-09-949-016-15921
11	38.2	5.9	7218	2	US-08-232-463-14
12	37.8	5.9	601	3	US-09-949-016-178415
13	37.8	5.9	99830	3	US-09-949-016-16859
14	37.6	5.8	601	3	US-09-949-016-163480
15	37.6	5.8	50000	3	US-09-662-254B-25
16	37.6	5.8	94593	3	US-08-545-528D-1
17	37.6	5.8	580073	3	US-09-949-016-15224
18	37.4	5.8	601	3	US-09-949-016-178416
19	37.2	5.8	601	3	US-09-949-016-163479
20	37.2	5.8	1844	3	US-09-123-912-88
21	37.2	5.8	1844	3	US-09-643-597-88
22	37.2	5.8	1844	3	US-09-480-884A-88
23	37.2	5.8	1844	3	US-09-542-615A-88
24	37.2	5.8	1844	3	US-09-606-421B-88

25	37.2	5.8	1844	3	US-09-221-107-88	Sequence 88, Appl
26	37.2	5.8	1844	3	US-09-466-396A-88	Sequence 88, Appl
27	37.2	5.8	1844	3	US-09-476-496A-88	Sequence 88, Appl
28	37.2	5.8	1844	3	US-09-630-940B-88	Sequence 88, Appl
29	37.2	5.8	1844	3	US-09-285-479-88	Sequence 88, Appl
30	37.2	5.8	1844	3	US-10-007-700-88	Sequence 14100, A
31	37.2	5.8	32721	3	US-09-949-016-14100	Sequence 14100, A
32	37.2	5.7	832	3	US-09-621-976-2813	Sequence 1813, Ap
33	36.8	5.7	48119	3	US-09-949-016-12003	Sequence 12003, A
34	36.8	5.7	48119	3	US-09-949-016-13177	Sequence 13177, A
35	36.8	5.7	50000	3	US-09-662-254B-26	Sequence 26, Appl
36	36.8	5.7	786431	3	US-09-751-389-3	Sequence 3, Appl
37	36.6	5.7	573	3	US-09-248-796A-6562	Sequence 6562, Ap
38	36.6	5.7	601	3	US-09-949-016-15821	Sequence 15821, A
39	36.4	5.6	38206	3	US-09-949-016-15827	Sequence 15827, A
40	36.4	5.6	124480	3	US-09-949-016-15921	Sequence 15921, A
41	36	5.6	1141	3	US-09-806-708B-22	Sequence 22, Appl
42	36	5.6	5619	3	US-09-799-451-241	Sequence 241, App
43	35.6	5.5	693	3	US-09-248-796A-1677	Sequence 1677, Ap
44	35.4	5.5	1818	3	US-09-107-532A-2423	Sequence 2423, Ap
45	35.4	5.5	232547	3	US-09-949-016-16603	Sequence 16603, A

ALIGNMENTS

RESULT 1
US-09-097-319A-1
; Sequence 1, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:
; APPLICANT: Attnley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Finkler, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Daykar
; APPLICANT: Petolino, Joseph P.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dowlingco Patent Department
; STREET: 9330 Zioneville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,319A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6550 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: exon

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/ LOCATION: 4201..4425
/ OTHER INFORMATION: /product= "Peroxidase"
/ FEATURE:
/ NAME/KEY: Intron
/ LOCATION: 4426..5058
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5059..5250
/ FEATURE:
/ NAME/KEY: Intron
/ LOCATION: 5251..5382
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5383..5548
/ FEATURE:
/ NAME/KEY: Intron
/ LOCATION: 5549..5649
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5650..6065
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: Join(4201..4425, 5059..5250, 5383..5547, 5649
/ LOCATION: ..6068)
/ US-09-097-319A-1
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Query Match 100.0%; Score 645; DB 3; Length 6550;

Best Local Similarity 100.0%; Pred. No. 9.9e-170; Indels 0; Gaps 0;

Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCAGAGTTCATATTCCTCTCTCTGTATGTTCTTTATATTAATGCTCTGCAAAAGCT 60
DB 4420 GTCAGAGTTCATATTCCTCTCTCTGTATGTTCTTTATATTAATGCTCTGCAAAAGCT 4479
QY 61 ATAAAGCTTGATCTGAGTATATATTAACAAGTTACTGACAAAGTTTGACTTTAG 120
DB 4480 ATAAAGCTTGATCTGAGTATATATTAACAAGTTACTGACAAAGTTTGACTTTAG 4539
QY 121 TCTTTTAACTATATGTTGGTGAATATAGATTATGAGTAATCCATGATGAGGTGGCAAG 180
DB 4540 TCTTTTAACTATATGTTGGTGAATATAGATTATGAGTAATCCATGATGAGGTGGCAAG 4599
QY 181 AGAATCATGAAGGCAAGATTAACGATGAAGCCATTACTAGCTTTGGCTGTATCAGACC 240
DB 4600 AGAATCATGAAGGCAAGATTAACGATGAAGCCATTACTAGCTTTGGCTGTATCAGACC 4659
QY 241 AATTAAGTTGAATGCACTTGTGCTAGCATGCTTAAGTATTGAAAAAGTATGAGGAGA 300
DB 4660 AATTAAGTTGAATGCACTTGTGCTAGCATGCTTAAGTATTGAAAAAGTATGAGGAGA 4719
QY 301 ATCTATATTTATTTGGGCTAAGCTTTTATGTTACTATGATTGATGAGAAAGCCATCATT 360
DB 4720 ATCTATATTTATTTGGGCTAAGCTTTTATGTTACTATGATTGATGAGAAAGCCATCATT 4779
QY 361 GCCCATCCAGCCCTTAATGTCCTCGGTGACATGATGAGCACTAATGATTATTTACT 420
DB 4780 GCCCATCCAGCCCTTAATGTCCTCGGTGACATGATGAGCACTAATGATTATTTACT 4839
QY 421 CTAATGTTCTCTTTTGAAGTGTCTGTAAGAATGTCCTTTTGAAGCACTGAGAG 480
DB 4840 CTAATGTTCTCTTTTGAAGTGTCTGTAAGAATGTCCTTTTGAAGCACTGAGAG 4899
QY 481 ATGTTTACTTAACCTAGTGGCAATGTTGAGACTCTGAGTGAAGCAATGAGCTCTGT 540
DB 4900 ATGTTTACTTAACCTAGTGGCAATGTTGAGACTCTGAGTGAAGCAATGAGCTCTGT 4959
QY 541 AATCTAGTCAACCACTACTCTGTAGTGTGTCTTAACTTAATCTTAATTCAGAGT 600
DB 4960 AATCTAGTCAACCACTACTCTGTAGTGTGTCTTAACTTAATCTTAATTCAGAGT 5019
QY 601 AGTAATTAACCAATCATTTTAACTGTTTACATGTGTAGGGCTGC 645
DB 5020 AGTAATTAACCAATCATTTTAACTGTTTACATGTGTAGGGCTGC 5064
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RESULT 2

US-09-643-971-1

; Sequence 1, Application US/09643971

; Patent No. 6699984

; GENERAL INFORMATION:

; APPLICANT: Ainley, Michael

; APPLICANT: Armstrong, Katherine

; APPLICANT: Belmar, Scott

; APPLICANT: Folkerts, Otto

; APPLICANT: Hopkins, Nicole

; APPLICANT: Menke, Michael A.

; APPLICANT: Paredino, Dayakar F.

; APPLICANT: Petolino, Joseph F.

; APPLICANT: Smith, Kelley

; APPLICANT: Woosley, Aaron

; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Dowelanco Patent Department

; STREET: 9330 Zionville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/643,971

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Stuart, Donald R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317 337 4816

; TELEFAX: 317 337 4847

; INFORMATION FOR SEQ. ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6550 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: exon

; LOCATION: 4201..4425

; OTHER INFORMATION: /product= "Peroxidase"

; FEATURE:

; NAME/KEY: Intron

; LOCATION: 4426..5058

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5059..5250

; FEATURE:

; NAME/KEY: Intron

; LOCATION: 5251..5382

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5383..5548

; FEATURE:

; NAME/KEY: Intron

; LOCATION: 5549..5649

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5650..6065

; FEATURE:

; NAME/KEY: CDS

; LOCATION: Join(4201..4425, 5059..5250, 5383..5547, 5649

; LOCATION: ..6068)

US-09-643-971-1

Query Match 100.0%; Score 645; DB 3; Length 6550;
Best Local Similarity 100.0%; Pred. No. 9.9e-170;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAAGTTCATATTCCTCTCTGTATGTTCTTTATATATACAGCTGTGCAAGCT 60
|||||
4420 GTCAAGTTCATATTCCTCTCTGTATGTTCTTTATATATACAGCTGTGCAAGCT 4479
61 ATAAAGCTTGATATCTGAGATATATATATACAGCTGTGCAAGCTTTGATCTTCAAG 120
4480 ATAAAGCTTGATATCTGAGATATATATATACAGCTGTGCAAGCTTTGATCTTCAAG 4539
121 TCTTTTAACTATATGTTGGTGAATATAGATTAAGATTAAGATTAAGATTAAGATTAAG 180
4540 TCTTTTAACTATATGTTGGTGAATATAGATTAAGATTAAGATTAAGATTAAGATTAAG 4599
181 AGAATGAAAGGCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 240
4600 AGAATGAAAGGCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 4659
241 AATTAATGAAATGCACTTGTGTAGATGCTTAAGATTAAGATTAAGATTAAGATTAAG 300
4660 AATTAATGAAATGCACTTGTGTAGATGCTTAAGATTAAGATTAAGATTAAGATTAAG 4719
301 ATTTATATATATTTGGCTAATCTTTATATATATATATATATATATATATATATATAT 360
4720 ATTTATATATATTTGGCTAATCTTTATATATATATATATATATATATATATATATAT 4779
361 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGAT 420
4780 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGAT 4839
421 CTATGTTCTCTTTTGAAGTCTGTATATATATATATATATATATATATATATATATAT 480
4840 CTATGTTCTCTTTTGAAGTCTGTATATATATATATATATATATATATATATATATAT 4899
481 ATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 540
4900 ATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 4959
541 AATCTACTGTCACCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 600
4960 AATCTACTGTCACCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 5019
601 AGTAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCA 645
5020 AGTAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCA 5064

RESULT 3

US-09-097-319A-19
Sequence 19, Application US/09097319A
Patent No. 6384207

GENERAL INFORMATION:

APPLICANT: Atley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Paredy, Dayakar
APPLICANT: Petolino, Joseph P.
APPLICANT: Smith, Kelley
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelance Patent Department
STREET: 9330 Zionville Road
CITY: Indianapolis
STATE: Indiana

COUNTRY: USA

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,319A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Stuart, Donald R

TELEPHONE: 317 337 4816

TELEFAX: 317 337 4816

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 9335 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA

US-09-097-319A-19

Query Match 100.0%; Score 645; DB 3; Length 9335;
Best Local Similarity 100.0%; Pred. No. 1.1e-169;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAAGTTCATATTCCTCTCTGTATGTTCTTTATATATACAGCTGTGCAAGCT 60
|||||
1758 GTCAAGTTCATATTCCTCTCTGTATGTTCTTTATATATACAGCTGTGCAAGCT 1817
61 ATAAAGCTTGATATCTGAGATATATATATACAGCTGTGCAAGCTTTGATCTTCAAG 120
1818 ATAAAGCTTGATATCTGAGATATATATATACAGCTGTGCAAGCTTTGATCTTCAAG 1877
121 TCTTTTAACTATATGTTGGTGAATATAGATTAAGATTAAGATTAAGATTAAGATTAAG 180
1878 TCTTTTAACTATATGTTGGTGAATATAGATTAAGATTAAGATTAAGATTAAGATTAAG 1937
181 AGAATGAAAGGCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 240
1938 AGAATGAAAGGCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1997
241 AATTAATGAAATGCACTTGTGTAGATGCTTAAGATTAAGATTAAGATTAAGATTAAG 300
1998 AATTAATGAAATGCACTTGTGTAGATGCTTAAGATTAAGATTAAGATTAAGATTAAG 2057
301 ATTTATATATATTTGGCTAATCTTTATATATATATATATATATATATATATATATAT 360
2058 ATTTATATATATTTGGCTAATCTTTATATATATATATATATATATATATATATATAT 2117
361 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGAT 420
2118 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGAT 2177
421 CTATGTTCTCTTTTGAAGTCTGTATATATATATATATATATATATATATATATATAT 480
2178 CTATGTTCTCTTTTGAAGTCTGTATATATATATATATATATATATATATATATATAT 2237
481 ATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 540
2238 ATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2297
541 AATCTACTGTCACCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 600
2298 AATCTACTGTCACCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2357
601 AGTAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCA 645
2358 AGTAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCAATCAATTAACCA 2402

RESULT 4
US-09-643-971-19
; Sequence 19, Application US/09643971
; Patent No. 669984
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Wooley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowlingco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,971
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; US-09-643-971-19

Query Match 100.0%; Score 645; DB 3; Length 935;
Best Local Similarity 100.0%; Pred. No. 1.1e-169;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAAGTTCAATTCCTCTCTGTTATGTTTATATTAATGCTGACAAAGCT 60
DB 1758 GTCAAGTTCAATTCCTCTCTGTTATGTTTATATTAATGCTGACAAAGCT 1817
QY 61 ATAAAGTTGATCGAGTATATTAATTAACAAGTTAGTACAAAGTTTGTACTTCAAG 120
DB 1818 ATAAAGTTGATCGAGTATATTAATTAACAAGTTAGTACAAAGTTTGTACTTCAAG 1877
QY 121 TCTTTAATATATGTTGGTCAATTAAGATTATGATTCATATGAAGGTTTGCAAG 180
DB 1878 TCTTTAATATATGTTGGTCAATTAAGATTATGATTCATATGAAGGTTTGCAAG 1937
QY 181 AGAATCATGAAGGCAAGATTAAGGATGAACCCATTAATGCTTTGGCTGTACAAAC 240
DB 1938 AGAATCATGAAGGCAAGATTAAGGATGAACCCATTAATGCTTTGGCTGTACAAAC 1997
QY 241 AATACTTGAATGCACTTGTGCTAGCATGCTTAAGTATTAAGAAAGGATGAGGAGA 300
DB 1998 AATACTTGAATGCACTTGTGCTAGCATGCTTAAGTATTAAGAAAGGATGAGGAGA 2057
QY 301 ATCTATATATTTTGGCTAATCTTGTATGATTAATGATGAGAAAGCCATCAATT 360

DB 2058 ATCTATATATTTTGGCTAATCTTGTATGATTAATGATGAGAAAGCCATCAATT 2117
QY 361 GCCATGCGAGCCCTAATGTCGGGAGCATGATGAGGACAGACTATTAATTACT 420
DB 2118 GCCATGCGAGCCCTAATGTCGGGAGCATGATGAGGACAGACTATTAATTACT 2177
QY 421 CTATGTCCTCTTTTGTAGTGTATTAAGATGCTTTTGTAGCCACTGGAAG 480
DB 2178 CTATGTCCTCTTTTGTAGTGTATTAAGATGCTTTTGTAGCCACTGGAAG 2237
QY 481 ATGTTACTTAACTTAAGCGGCAATGATGAGCTCTAGTCAACGATGCTGTGT 540
DB 2238 ATGTTACTTAACTTAAGCGGCAATGATGAGCTCTAGTCAACGATGCTGTGT 2297
QY 541 AATCTAGTCACCACTACTGTAAGTGTGCTTAACTTAACCTTAATTCAGAGGCT 600
DB 2298 AATCTAGTCACCACTACTGTAAGTGTGCTTAACTTAACCTTAATTCAGAGGCT 2257
QY 601 AGTAATTAACCAATCAATTACAACACTGTTACATGATGAGGCTGC 645
DB 2358 AGTAATTAACCAATCAATTACAACACTGTTACATGATGAGGCTGC 2402

RESULT 5
US-09-949-016-14606/c
; Sequence 14606, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14606
; LENGTH: 83178
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14606

Query Match 6.8%; Score 43.8; DB 3; Length 83178;
Best Local Similarity 53.1%; Pred. No. 0.091;
Matches 93; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 37 TATATTACATGCTCTGCAAAAGCTATTAAGCTGATACGATATATTAACAAGTTA 96
DB 60785 TCTTTGACTTGCCTGAGGAAGCACTGACCATTTATTTAATCTATTAATCAATTA 60726
QY 97 GTACACAAGTTTGTACTCAAGCTTTTAACTATATATGTTGGCAATAAGATTATGAG 156
DB 60725 ACTTCAATCAATGATGATCAATTAATTAATCTTGAATGATCAATTAATTAATTA 60666
QY 157 TAAATCATGAAGGTTGTCAGAGAGAAACATGAAGGCAAGTAACCGATGAG 211
DB 60665 TAAATCATGAAGGTTGTTTCAACAGAAATTAATGATGATTTAAACAGTTCA 60611

RESULT 6
US-09-949-016-103411/c
; Sequence 103411, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 103411
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-103411

Query Match 6.7%; Score 43.4; DB 3; Length 601;
Best Local Similarity 52.6%; Pred. No. 0.022;
Matches 92; Conservative 1; Mismatches 82; Indels 0; Gaps 0;

QY 37 TATATACATGCTCTGACAAAGCTATTAAGCTTGAATCTGACATATATATTAACAAGTTA 96
DB 370 TCTTGAATGCTGTAGAGGACGACGACATTTATTTAATCTGATCTATATCCATATA 311
QY 97 GCTACACAGTTTGTACTTCAAGTCTTTAATCTATATGTGGTCAATAGATTATGAG 156
DB 310 ACTTCATCATTAAGGACTGAAATATCTTGAATGATCCCTTAACAAATTTCTGTATGG 251
QY 157 TAATCATATGAGGTGTTGCAAGAGAACATGAAGCAAGATTAACGATGA 211
DB 250 TATATATATGCTGTGTTTCAACAGAAATGATGATTTTAAAGATTCA 196

RESULT 7
US-09-662-254B-23/c
Sequence 23, Application US/09662254B
Patent No. 6931145
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: LI, YI
TITLE OF INVENTION: Bowden, Allison Louise
TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
TITLE OF INVENTION: Vertebrate Cells
FILE REFERENCE: UF-221C1X1
CURRENT APPLICATION NUMBER: US/09/662,254B
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/086,651
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patent version 3.1
SEQ ID NO 23
LENGTH: 50000
TYPE: DNA
ORGANISM: Ambacta moorei entomopoxvirus
US-09-662-254B-23

Query Match 6.6%; Score 42.8; DB 3; Length 50000;
Best Local Similarity 45.9%; Pred. No. 0.15;
Matches 166; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 27 TTAGTCTTTATATATACATGCTCTGACAAAGCTATTAAGCTTGAATCTGACATATATA 86
DB 11134 TGAATATAATGTAATATATATATATATATATATATATATATATATATATATA 11075
QY 87 TAAACAGTAGACACACAGTTTGTACTTCAAGTCTTTAATCTATATGTGGTCAATA 146
DB 11074 TAAATATATAAAGAAACAGATTTTATCTGTAATATTTTAAATTTTAAACAAAGTATATC 11015
QY 147 AGATTATGATATCATATATGAGTGTGCAAGAGAACATGAAGCAAGATTAACG 206

DB 11014 TTTATATCCGACGTTTGCAACACAGTTGAAAAAATCAAAATATATATATATATAT 10955
QY 207 ATGACCCATTACTACTGCTTGGCTGATACAGACCAATTAATGCACTTGTGTAG 266
DB 10954 AATATATATATATATGCAATCTTTGATGTATATATATATATATATATATATAGCA 10895
QY 267 CAGCCCTAAGTATATATAAAGGATGAGATGGGAAATCTATATATTTGGCTAATCTT 326
DB 10894 CAATACGTAATAATAATAATTAACGTTATATATATATATATATATATATATACAAA 10835
QY 327 TAGTACTATATGATGAT 344
DB 10834 AACTATATATATTTTCAAT 10817

RESULT 8
US-09-806-708B-23
Sequence 23, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent version 3.0
SEQ ID NO 23
LENGTH: 1055
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)-(1055)
OTHER INFORMATION: consensus sequence of A.T. and L.A. FAE1 promoters
US-09-806-708B-23

Query Match 6.3%; Score 40.8; DB 3; Length 1055;
Best Local Similarity 19.8%; Pred. No. 0.14;
Matches 90; Conservative 120; Mismatches 244; Indels 0; Gaps 0;

QY 58 GCTATAAGCTGATACGACGATATATATACAACTGATGACACAACTTTGTACTTC 117
DB 45 RCYARRGKMTTAYVMTATATGTTGAAATRWAAAKTKRKMCSYAMNNAATTTCTARK 104
QY 118 AAGCTTTTAACTATATATGTGGCAATAGATTAAGATTAATCCATATGAAGTGTGC 177
DB 105 WRTGTWMTKTNNAATGTRMTGWTGWTNNNGSTMTWARRYKTRRWCTYAMVYASWAG 164
QY 178 AAGAGAACATGAAGGCAAGATTAACGATGAACCATTAATGCTGATGATCAG 237
DB 165 NSTRTTYYTKMKMKCKRSAPARTRBGRATWATMAARCTGTAMAAATMTN 224
QY 238 ACCAATTAATGAAATGCACTGTGCTAGACATGCTTAAGTATTAAGAAAGTATGAG 297
DB 225 NNNNAKAAKRAATWGMRAKSNCTCTAGTTTBRATCCAAATCGAGMATKKKWTSA 284
QY 298 AGAATCTATATATTTTGGCTAATCTTTAGTACTATATGATGATGAAAGCTATAC 357
DB 285 AAGMTNNNNNNNNNTTAKAATTAATAAAMWMSATTTWAAAMTSRKTTWYGRKTAAMNN 344
QY 358 ATGGCCATGCGACCCCTAATGTCCTGCTGACATGATGAGCAGATGATATATTT 417
DB 345 GTTCATWMAATWTKMKMKTKGTTTMMNNNGRTYTGTTTAKMAATTTTAKANNCTAAKMK 404
QY 418 ACTCTATGTTGCTCTTTTGAAGTGTATATAGATGTCCTTTTGAAGCCTGAG 477
DB 405 TCTMNTTAAKATTTWATCWKSMNTGTSYRAAAYTVAAMWTRVYANNNTTWTWK 464
QY 478 AAGATTTTAATTAATCTATGATGCGCAATGATG 511


```
/ APPLICATION NUMBER: US/07/935,313
/ FILING DATE:
/ APPLICATION NUMBER: EP 91 114 300.6
/ FILING DATE: 26-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 30472/114 IMMU
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7218 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: pTZpct-F18
/ US-08-232-463-14
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Query Match 5.9%; Score 38.2; DB 2; Length 7218;
Best Local Similarity 6.5%; Pred. No. 1.4;
Matches 22; Conservative 17; Mismatches 144; Indels 0; Gaps 0;
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QY 302 TCATATATTATTTGGCTACTCTTCTTACTTACTTGAATGAGAAAGCTACCTATG 361
DB 1142 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1201
QY 362 CCCATGCGACCCCTAATGCGCGATGATGAGCGACGATCTAATGATTAATTAATG 421
DB 1202 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1261
QY 422 TATGTCTCTCTTTTGTAGTGTGTAATGATGCTTTTGTAGCCACTGAGAGAA 481
DB 1262 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1321
QY 482 TGTCTACTTACTCTAGTGGCAATGATTTGAGCTCTCACTGCAAGCATGCTCTGTA 541
DB 1322 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1381
QY 542 ATCTACGTGACACACTGCTAGTGTGCTTAACCTAATGATTAATGATGAGTGA 601
DB 1382 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1441
QY 602 GATATTACCAATGATTTACCAACCTGTTACATGTA 638
DB 1442 ATCTTCTATCTCTTTTACTACTGATGATAGTGA 1478
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RESULT 12
US-09-949-016-178415/C
/ Sequence 178415, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FaSeq for Windows Version 4.0
/ SEQ ID NO 178415
/ LENGTH: 601
/ TYPE: DNA
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/ ORGANISM: Human
/ US-09-949-016-178415
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Query Match 5.9%; Score 37.8; DB 3; Length 601;
Best Local Similarity 50.8%; Pred. No. 0.81;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
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QY 134 TGTGTGCAATTAAGTATTAAGTATCAATGAGGTGTCAGAGAACTGAAGG 193
DB 526 TGTACTGAAGTCAGAAATCAGAAATTAAGTCTAGAGGTTGCAACAGAGAAATTAAGG 467
QY 194 CAAGATTAACGAGATGACCATTAAGCTTTGCTGTATCAGACCAATTAAGTGAAT 253
DB 466 ACAAAATTAATGGAATATCAGTTACTTAAGATCAGATCTATTAATCTTAAGTCTTAC 407
QY 254 GCACTGTGCTAGACGCTTAAGTATTAAGAAAGTGAAGATGGAATCTATATTA 310
DB 406 GGCTATTGATCAATTCAGACAGCATCACCAAAACATGGAAGATTCATGTATCTTA 350
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RESULT 13

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US-09-949-016-16859/C
/ Sequence 16859, Application US/09949016
/ Patent No. 6812339
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/ GENERAL INFORMATION:
```

```
/ APPLICANT: VENTER, J. Craig et al.
```

```
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
/ FILE REFERENCE: CL001307
```

```
/ CURRENT APPLICATION NUMBER: US/09/949,016
```

```
/ PRIOR FILING DATE: 2000-04-14
```

```
/ PRIOR APPLICATION NUMBER: 60/241,755
```

```
/ PRIOR FILING DATE: 2000-10-20
```

```
/ PRIOR APPLICATION NUMBER: 60/237,768
```

```
/ PRIOR FILING DATE: 2000-10-03
```

```
/ PRIOR APPLICATION NUMBER: 60/231,498
```

```
/ PRIOR FILING DATE: 2000-09-08
```

```
/ NUMBER OF SEQ ID NOS: 207012
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/ SOFTWARE: FaSeq for Windows Version 4.0
```

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/ SEQ ID NO 16859
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/ LENGTH: 99830
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/ TYPE: DNA
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/ ORGANISM: Human
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/ FEATURE: misc_feature
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/ NAME/KEY: (1)...(99830)
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/ LOCATION: (1)...(99830)
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/ OTHER INFORMATION: n = A,T,C or G
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US-09-949-016-16859
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Query Match 5.9%; Score 37.8; DB 3; Length 99830;
Best Local Similarity 50.8%; Pred. No. 4.5;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
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QY 134 TGTGTGCAATTAAGTATTAAGTATCAATGAGGTGTCAGAGAACTGAAGG 193
DB 7667 TGTACTGAAGTCAGAAATCAGAAATTAAGTCTAGAGGTTGCAACAGAGAAATTAAGG 7608
QY 194 CAAGATTAACGAGATGACCATTAAGCTTTGCTGTATCAGACCAATTAAGTGAAT 253
DB 7607 ACAAAATTAATGGAATATCAGTTACTTAAGATCAGATCTATTAATCTTAAGTCTTAC 7548
QY 254 GCACTGTGCTAGACGCTTAAGTATTAAGAAAGTGAAGATGGAATCTATATTA 310
DB 7547 GGCTATTGATCAATTCAGACAGCATCACCAAAACATGGAAGATTCATGTATCTTA 7491
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RESULT 14

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US-09-949-016-163480/C
/ Sequence 163480, Application US/09949016
/ Patent No. 6812339
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/ GENERAL INFORMATION:
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/ APPLICANT: VENTER, J. Craig et al.
```

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/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CLO01307
:
: CURRENT APPLICATION NUMBER: US/09/949,016
:
: CURRENT FILING DATE: 2000-04-14
:
: PRIOR APPLICATION NUMBER: 60/241,755
:
: PRIOR FILING DATE: 2000-10-20
:
: PRIOR APPLICATION NUMBER: 60/237,768
:
: PRIOR FILING DATE: 2000-10-03
:
: PRIOR APPLICATION NUMBER: 60/231,498
:
: PRIOR FILING DATE: 2000-09-08
:
: NUMBER OF SEQ ID NOS: 207012
:
: SOFTWARE: FASTSEQ for Windows Version 4.0
:
: SEQ ID NO 163480
:
: LENGTH: 601
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: TYPE: DNA
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: ORGANISM: Human
:
: US-09-949-016-163480

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Query Match	5.8%	Score	37.6	DB	3	Length	601
Best Local Similarity	49.5%	Pred. No.	0.92				
Matches	97	Conservative	0	Mismatches	99	Indels	0
						Gaps	0

Qy	33	TCCTTAATATACAGCTCTGCAAAAGCATATAAGCTATATCTGACAGATATATATACAA	92
Db	240	TTTTTGGTCTCTTCTGAAGTAATATTTGCATGCTAACAAAGATATTTTCATTAAATAA	181
Qy	93	GTTAGCTACACAAGTTTTGTACTTCAGATCTTTTAACTATATGTTGTGCATATAGATTA	152
Db	180	ATATTTTAGTATAGATTTGGTTTTTAAAGTTTTCTTTAGTTGTTTAAACAATTTA	121
Qy	153	TGAGTATCCATATGAAAGTGTTCAGAAAGAACATGAAAGCCAAAGATAAACGATGAC	212
Db	120	ATTTTAAACATTCGATATATGTTAAACAGATCATATAGGAGAAATGATTTGGGGTTT	61
Qy	213	CCATTACTAGCTTTGG	228
Db	60	CATTTTAAAGATTTAG	45

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RESULT 15
US-09-662-254B-25/C
Sequence 25, Application US/09662254B
Patent No. 6933145
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Li, Yi
APPLICANT: Bawden, Alison Louise
TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
FILE REFERENCE: UF-221C1X1
CURRENT APPLICATION NUMBER: US/09/662,254B
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/086,651
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 50000
TYPE: DNA
ORGANISM: Ambacta moorei entomopoxvirus
US-09-662-254B-25

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Query Match	5.8%	Score 37.6;	DB 3;	Length 5000;
Best Local Similarity	45.8%	Pred. No. 4.1;		
Matches 130; Conservative	0;	Mismatches 154;	Indels 0;	Gaps 0;

QY 53 ACAAAGCATTAAGCTTGATCTGCAGATATATATAACAAGTTAGCTACACAAGTTTGT 112

Db 33481 ATTAATAATATTAATTTTCATATGTAATAAATAATATATTAACATCATGATATATTATGATCTCA 33422

QY 113 ACTTCAAGTCTTTTAACATATATGTTGGTGCATAAGATTATGAGTAATCCATATGAAGGT 172

[illegible]

Search completed: February 12, 2006, 00:05:55
Job time : 182 secs

Search completed: February 12, 2006, 00:05:55
Job time : 182 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:30:15 ; Search time 3911 Seconds
(without alignments)
9374.591 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645
Sequence: 1 GTCAGAGTCGATTCGCTT.....TGTTCATGTCGAGGCTGC 645

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_dr:*
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10: gb_str:*
11: gb_gy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pli:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	645	100.0	6550	6	BD132692
2	645	100.0	6550	6	AR208995
3	645	100.0	6550	6	AR482064
4	645	100.0	9335	6	BD132709
5	645	100.0	9335	6	AR209012
6	645	100.0	9335	6	AR482081
7	46.2	7.2	2000	6	AX553393
8	45.8	7.1	12028	2	AE001412
9	44.4	6.9	13383	2	AE001374
10	44.4	6.9	12866	5	BX510935
11	43.8	6.8	138363	6	CQ869722
12	43.8	6.8	210331	8	AL157402
13	42.8	6.6	1525	2	AY701198
14	42.8	6.6	50000	6	AX392733
15	42.8	6.6	232392	13	AF250284
16	42.2	6.5	155952	8	AC004534
17	42	6.5	183246	14	AC118486
18	41.8	6.5	92620	15	AB026636

19	41.8	6.5	153232	5	AL772263	AL772263 Zebrafish
20	41.8	6.5	158330	8	AC025599	AC025599 Homo sapi
21	41.8	6.5	195070	14	AC068995	AC068995 Homo sapi
22	41.6	6.4	127270	8	AC004740	AC004740 Homo sapi
23	41.6	6.4	196260	14	AC136415	AC136415 Rattus no
24	41.6	6.4	246134	14	AC135647	AC135647 Rattus no
25	41.4	6.4	157811	8	AC079071	AC079071 Homo sapi
26	41.4	6.4	168500	14	AC021796	AC021796 Homo sapi
27	41	6.4	69471	14	AC117400	Continuation (4 of
28	41	6.4	110000	15	AP008218	Continuation (106
29	41	6.4	112916	15	CNS08C9X	AL772419 Oryza sat
30	41	6.4	130672	15	CNS08C9Z	AL772421 Oryza sat
31	41	6.4	147359	8	AP002345	AP002345 Homo sapi
32	40.8	6.3	1055	6	AR576681	AR576681 Sequence
33	40.8	6.3	1055	6	AX083745	AX083745 Sequence
34	40.8	6.3	75589	8	BS000034	BS000034 Pan trogl
35	40.8	6.3	145274	8	AC135559	AC135559 Homo sapi
36	40.8	6.3	348034	2	CR382400	CR382400 Plasmid
37	40.6	6.3	704	10	BV475571	BV475571 GS91P6330
38	40.6	6.3	1532	2	AY701231	AY701231 Orconecte
39	40.6	6.3	155935	8	AC006442	AC006442 Homo sapi
40	40.6	6.3	157028	8	AL139000	AL139000 Human DNA
41	40.6	6.3	225038	14	AC111507	AC111507 Rattus no
42	40.6	6.3	236550	14	AC103061	AC103061 Rattus no
43	40.4	6.3	97751	8	AC084257	AC084257 Homo sapi
44	40.4	6.3	155821	8	AC027043	AC027043 Homo sapi
45	40.4	6.3	169262	8	AC090569	AC090569 Homo sapi

ALIGNMENTS

RESULT 1	BD132692	BD132692	6550 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD132692	Regulatory sequences for transgenic plants.				
DEFINITION	BD132692	BD132692				
ACCESSION	BD132692.1	GI:23227637				
VERSION	JP 2002504824-A/1.					
KEYWORDS						
SOURCE		synthetic construct				
ORGANISM		other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 6550)					
AUTHORS	Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N., Menke,M.A., Paredy,D., Petolino,J.F., Smith,K. and Woosley,A.					
TITLE	Regulatory sequences for transgenic plants					
JOURNAL	Patent: JP 2002504824-A 1 12-FEB-2002;					
COMMENT	DOM AGRSCIENCES LLC					
	PN JP 2002504824-A/1					
	PD 12-FEB-2002					
	PF 10-JUN-1998 JP 199503094					
	PR 12-JUN-1997 US 60/0649752					
	PI MICHAEL AINLEY,KATHERINE ARMSTRONG,SCOTT BELMAR,OTTO FOLKERTS,PI NICOLE HOPKINS,MICHAEL A MENKE,DAYAKAR PAREDDY,JOSEPH F PETOLINO,					
	PI KELLEY SMITH,AARON WOOSLEY					
	PC C12N15/53, C12N15/82, A01H5/00					
	CC Strandedness: Double;					
	CC Topology: Linear;					
	CC /products='peroxidase'					
	FH Key	Location/Qualifiers				
	FT exon	4201..4425				
	FT intron	4426..5058				
	FT exon	5059..5250				
	FT intron	5251..5382				
	FT exon	5383..5548				
	FT intron	5549..5649				
	FT exon	5650..6065				
	FT CDS					
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	join(4201..4425,5059..5250,5383..5547,5649..6068)					
FEATURES	Location/Qualifiers					
source	1..6550					

ORIGIN

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 100.0%; Score 645; DB 6; Length 6550;

Best Local Similarity 100.0%; Pred. No. 8.6e-134;

Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCAGGTTCAATTCCTGCTTCTCTGTATGCTTTATATTCATAGCTCTGCAAGCT 60
DB 4420 GTCAGGTTCAATTCCTGCTTCTCTGTATGCTTTATATTCATAGCTCTGCAAGCT 4479
QY 61 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 120
DB 4480 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 4539
QY 121 TCTTTTAACTATATGTTGGTGCATTAAGATTATGATATCCATATGAAGGTGTCAG 180
DB 4540 TCTTTTAACTATATGTTGGTGCATTAAGATTATGATATCCATATGAAGGTGTCAG 4599
QY 181 AGAACAATGAAGGCAAAAGATTAACCGATGAACCCATTACTAGCTTGGCTGTATCAGACC 240
DB 4600 AGAACAATGAAGGCAAAAGATTAACCGATGAACCCATTACTAGCTTGGCTGTATCAGACC 4659
QY 241 AATTAATCTGAAATGCACTTGTGCTAGCATGCTTAAGTAATTAAGAAAGTATGGAGA 300
DB 4660 AATTAATCTGAAATGCACTTGTGCTAGCATGCTTAAGTAATTAAGAAAGTATGGAGA 4719
QY 301 ATCTATATTAATTTTGGCTAACTTCTTTAGTTACTATTAATTAAGAAAGCTTACCATT 360
DB 4720 ATCTATATTAATTTTGGCTAACTTCTTTAGTTACTATTAATTAAGAAAGCTTACCATT 4779
QY 361 GCCCATGCGAGCCCTAATGTCCTGGTGCATGATTTGGCCAGTACTATGATTAATTACT 420
DB 4780 GCCCATGCGAGCCCTAATGTCCTGGTGCATGATTTGGCCAGTACTATGATTAATTACT 4839
QY 421 CTAATGTTCTCCTTTTGAAGTGTGTAAGATGTCCTTTTGAAGCACTCGAAG 480
DB 4840 CTAATGTTCTCCTTTTGAAGTGTGTAAGATGTCCTTTTGAAGCACTCGAAG 4899
QY 481 ATGTTTAACTTAACCTAGTGCAGATGATTTGAGCTCTCAGTGCAACGCAATGCTCTGT 540
DB 4900 ATGTTTAACTTAACCTAGTGCAGATGATTTGAGCTCTCAGTGCAACGCAATGCTCTGT 4959
QY 541 AATCTACTGTCAACCACTACTCTGTAAGTGTGCTTAACTCTAACTATCCAGTGGCT 600
DB 4960 AATCTACTGTCAACCACTACTCTGTAAGTGTGCTTAACTCTAACTATCCAGTGGCT 5019
QY 601 AGTAATTAACCAATCAATTAACAACCTGTACATGTGAGGGCTGC 645
DB 5020 AGTAATTAACCAATCAATTAACAACCTGTACATGTGAGGGCTGC 5064
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RESULT 2
LOCUS AR208995 6550 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6384207.
ACCESSION AR208995
VERSION AR208995.1 GI:21510295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 6550)
AUTHORS Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N.,
Menke,M.A., Pareddy,D., Petolino,J.F., Smith,K. and Woosley,A.

TITLE Regulatory sequences for transgenic plants
JOURNAL Patent: US 6384207-A 1 07-MAY-2002;
FEATURES Location/Qualifiers

source 1..6550
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 645; DB 6; Length 6550;

Best Local Similarity 100.0%; Pred. No. 8.6e-134;

Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCAGGTTCAATTCCTGCTTCTCTGTATGCTTTATATTCATAGCTCTGCAAGCT 60
DB 4420 GTCAGGTTCAATTCCTGCTTCTCTGTATGCTTTATATTCATAGCTCTGCAAGCT 4479
QY 61 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 120
DB 4480 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 4539
QY 121 TCTTTTAACTATATGTTGGTGCATTAAGATTATGATATCCATATGAAGGTGTCAG 180
DB 4540 TCTTTTAACTATATGTTGGTGCATTAAGATTATGATATCCATATGAAGGTGTCAG 4599
QY 181 AGAACAATGAAGGCAAAAGATTAACCGATGAACCCATTACTAGCTTGGCTGTATCAGACC 240
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QY 241 AATTAATCTGAAATGCACTTGTGCTAGCATGCTTAAGTAATTAAGAAAGTATGGAGA 300
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QY 301 ATCTATATTAATTTTGGCTAACTTCTTTAGTTACTATTAATTAAGAAAGCTTACCATT 360
DB 4720 ATCTATATTAATTTTGGCTAACTTCTTTAGTTACTATTAATTAAGAAAGCTTACCATT 4779
QY 361 GCCCATGCGAGCCCTAATGTCCTGGTGCATGATTTGGCCAGTACTATGATTAATTACT 420
DB 4780 GCCCATGCGAGCCCTAATGTCCTGGTGCATGATTTGGCCAGTACTATGATTAATTACT 4839
QY 421 CTAATGTTCTCCTTTTGAAGTGTGTAAGATGTCCTTTTGAAGCACTCGAAG 480
DB 4840 CTAATGTTCTCCTTTTGAAGTGTGTAAGATGTCCTTTTGAAGCACTCGAAG 4899
QY 481 ATGTTTAACTTAACCTAGTGCAGATGATTTGAGCTCTCAGTGCAACGCAATGCTCTGT 540
DB 4900 ATGTTTAACTTAACCTAGTGCAGATGATTTGAGCTCTCAGTGCAACGCAATGCTCTGT 4959
QY 541 AATCTACTGTCAACCACTACTCTGTAAGTGTGCTTAACTCTAACTATCCAGTGGCT 600
DB 4960 AATCTACTGTCAACCACTACTCTGTAAGTGTGCTTAACTCTAACTATCCAGTGGCT 5019
QY 601 AGTAATTAACCAATCAATTAACAACCTGTACATGTGAGGGCTGC 645
DB 5020 AGTAATTAACCAATCAATTAACAACCTGTACATGTGAGGGCTGC 5064
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RESULT 3
LOCUS AR482064 6550 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 1 from patent US 6699964.
ACCESSION AR482064
VERSION AR482064.1 GI:47244032
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 6550)
AUTHORS Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N.,
Menke,M.A., Pareddy,D., Petolino,J.F., Smith,K. and Woosley,A.

TITLE Regulatory sequences for transgenic plants
JOURNAL Patent: US 6699964-A 1 02-MAR-2004;
FEATURES Location/Qualifiers

source 1..6550
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match	100.0%	Score 645	DB 6	Length 6550
Beet Local Similarity	100.0%	Pred. No. 8.6e-134		
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			Gaps	0
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QY	61	ATAAAGCTTGATACTGCAGATATATATAACAAGTTAGTACACAAGTTTGTACTTCAAG	120	
Db	4480	ATAAAGCTTGATACTGCAGATATATATATAACAAGTTAGTACACAAGTTTGTACTTCAAG	4539	
QY	121	TCCTTTAATCTATATGTTGGTGCATAAAGATTATGATATATCATATGAAAGTGTGCAAG	180	
Db	4540	TCCTTTAATCTATATGTTGGTGCATAAAGATTATGATATATCATATGAAAGTGTGCAAG	4599	
QY	181	AGAACATGAAAGGCAAAAGATTAACGGATGAAGCCCATTACTAGAGTTGGCTGATCAGAC	240	
Db	4600	AGAACATGAAAGGCAAAAGATTAACGGATGAAGCCCATTACTAGAGTTGGCTGATCAGAC	4658	
QY	241	AATAACCTGAAATGCACTTGTGCTAGATGCTCCTAAGTATTAAGAAAGGTAGCATGGAGA	300	
Db	4660	AATAACCTGAAATGCACTTGTGCTAGATGCTCCTAAGTATTAAGAAAGGTAGCATGGAGA	4719	
QY	301	ATCTATATATATTTGGCTAATCTTCTTATGTTATTAATGATGATGAAAGCTTACATT	360	
Db	4720	ATCTATATATATTTGGCTAATCTTCTTATGTTATTAATGATGATGAAAGCTTACATT	4779	
QY	361	GCCCATGCGACGCCCTAATGTCGCCGTGACATGATTGACCGATATGATTAATTAATCT	420	
Db	4780	GCCCATGCGACGCCCTAATGTCGCCGTGACATGATTGACCGATATGATTAATTAATCT	4839	
QY	421	CTATTGTTCTCCTTTTGTGAGTGTGTTAAGATGTCCTTTTGTGACCACTGAGAG	480	
Db	4840	CTATTGTTCTCCTTTTGTGAGTGTGTTAAGATGTCCTTTTGTGACCACTGAGAG	4899	
QY	481	ATGTTTACTTAACTTATGTCGCAATGATTGAGCTCTCAGTGCACGACATGTGCTGT	540	
Db	4900	ATGTTTACTTAACTTATGTCGCAATGATTGAGCTCTCAGTGCACGACATGTGCTGT	4959	
QY	541	AATCAGCTGACCACTACCTGATGATGATGCTTAACTGTAATCTATTCACAGTGGCT	600	
Db	4960	AATCAGCTGACCACTACCTGATGATGATGCTTAACTGTAATCTATTCACAGTGGCT	5019	
QY	601	AGTAATTACCAATCTATTACAAACCTGTTACATGATGAGGCTGC	645	
Db	5020	AGTAATTACCAATCTATTACAAACCTGTTACATGATGAGGCTGC	5064	
RESULT 4				
LOCUS	BD132709	9335 bp	DNA	linear
DEFINITION	Regulatory sequences for transgenic plants.			
ACCESSION	BD132709			
VERSION	BD132709.1	GI:23227654		
KEYWORDS	JP 2002504824-A/18.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	Other sequences; artificial sequences.			
AUTHORS	1 (bases 1 to 9335)			
	Atalley, M., Armstrong, K., Belmar, S., Folkerts, O., Hopkins, N.,			
	Meike, M.A., Paredy, D., Petrolino, J.F., Smith, K., and Woosley, A.			
TITLE	Regulatory sequences for transgenic plants			
JOURNAL	Patent: JP 2002504824-A 18 12-FEB-2002;			
COMMENT	DOI: 10.26434/chemrxiv-2024-18			
	PN JP 2002504824-A/18			
	PD 12-FEB-2002			
	PF 10-JUN-1998 JP 1999503094			
	PR 12-JUN-1997 US 60/049752			
	PI MICHAEL, ATINLEY, KATHERINE ARMSTRONG, SCOTT BELMAR, OTTO FOLKERTS,			
	PI NICOLE HOPKINS, MICHAEL A MENKE, DAYAKAR PAREDDY, JOSEPH F PI			
	PETROLINO,			
	PI KELLEY SMITH, AARON WOOSLEY			

	PC	C12N15/53,C12N15/82,A0H5/00
	CC	Strandedness: Double;
	CC	Topology: Circular;
FEATURES	FH	Key Location/Qualifiers.
source		location/Qualifiers 1..9335 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
ORIGIN		
Query Match	100.0%; Score 645; DB 6; Length 9335;	
Best Local Similarity	100.0%; Pred. No.7.8e-134; Mismatches 0; Indels 0; Gaps 0;	
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Oy	61	ATAAAGCTTGATCTGCAAGTAAATATPAACAAGTTAGCTACACAAAGTTTGTACTTCAAG 120
Db	1818	ATAAAGCTTGATCTGCAAGTAAATATPAACAAGTTAGCTACACAAAGTTTGTACTTCAAG 1877
Oy	121	TCTTTTAATTAATGTTGGTGAATTAAGATTAGAAGTAATCCAAATGAAGTGTTCGAAG 180
Db	1878	TCTTTTAATTAATGTTGGTGAATTAAGATTAGAAGTAATCCAAATGAAGTGTTCGAAG 1937
Oy	181	AGAACATGAAGAAGCAAAGATTAACGAGATGAACCATTAATAGCTTTGGCTGTATCAGACC 240
Db	1938	AGAACATGAAGAAGCAAAGATTAACGAGATGAACCATTAATAGCTTTGGCTGTATCAGACC 1997
Oy	241	AATAACTTGAANAATGCACTGTGTAGCATAGCTTAAGATTAGAAAAGGTAGCATGGGAGA 300
Db	1998	AATAACTTGAANAATGCACTGTGTAGCATAGCTTAAGATTAGAAAAGGTAGCATGGGAGA 2057
Oy	301	ATCTAATTAATTTGGCTAACTTTTAACTTAATTAATTAATTAATTAATTAATTAATTAAT 360
Db	2058	ATCTAATTAATTTGGCTAACTTTTAACTTAATTAATTAATTAATTAATTAATTAATTAAT 2117
Oy	361	GCCCATGCCAGCCCTTAATGTCGGGTGACATGATGAGCCAGTACTAATTAATTAATTAAT 420
Db	2118	GCCCATGCCAGCCCTTAATGTCGGGTGACATGATGAGCCAGTACTAATTAATTAATTAAT 2177
Oy	421	CTATTGTTCTCTTTTGTAGTGTCTAATAGATGTCCTTTTTTGTAGCCAATGAGAAAG 480
Db	2178	CTATTGTTCTCTTTTGTAGTGTCTAATAGATGTCCTTTTTTGTAGCCAATGAGAAAG 2237
Oy	481	ATGTTTAATTAATCTTAGTGTGCGCAATGATGAGCTCTCAGTGCAAGCATGTGCTCTGT 540
Db	2238	ATGTTTAATTAATCTTAGTGTGCGCAATGATGAGCTCTCAGTGCAAGCATGTGCTCTGT 2297
Oy	541	AATCTACATGACACACATCTGTAGTGTGCGCTTAACTCTAACTAATTCACAGTGGCT 600
Db	2298	AATCTACATGACACACATCTGTAGTGTGCGCTTAACTCTAATTCACAGTGGCT 2357
Oy	601	AGTAATTAACCAATCAATTACAACACTGTTACATGTGAGGGCTGC 645
Db	2358	AGTAATTAACCAATCAATTACAACACTGTTACATGTGAGGGCTGC 2402
RESULT 5		
AR209012	9335 bp	DNA linear PAT 20-JUN-2002
LOCUS		
DEFINITION	Sequence 19 from patent US 6584207.	
ACCESSION	AR209012	
VERSION	AR209012.1	GI:21510317
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 9335)	
AUTHORS	Anley,M., Armstrong,K., Belnar,S., Folkerbs,O., Hopkins,N., Meike,M.A., Pareddy,D., Petolino,J.F., Smith,K. and Woosley,A.	

TITLE Regulatory sequences for transgenic plants
JOURNAL Patent: US 6384207-A 19 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..9335
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 645; DB 6; Length 9335;
Best Local Similarity 100.0%; Pred. No. 7,8e-134;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAGAGTTCAATTCGCTTCCCTGCTGTTATGTTCTTATATTCATGCTCTGCAAAAGCT 60
DB 1758 GTCAAGTTCAATTCGCTTCCCTGCTGTTATGTTCTTATATTCATGCTCTGCAAAAGCT 1817
QY 61 ATAAAGTTGATCTGCAATATATTAACAAGTTAGTACACAAAGTTTGTACTTCAAG 120
DB 1818 ATAAAGTTGATCTGCAATATATTAACAAGTTAGTACACAAAGTTTGTACTTCAAG 1877
QY 121 TCTTTTAACTATATGTTGGTGCATTAATGAGTAATCCATATGAAAGTTGCAAG 180
DB 1878 TCTTTTAACTATATGTTGGTGCATTAATGAGTAATCCATATGAAAGTTGCAAG 1937
QY 181 AGAACAATGAAGCAAAAGATTAACGATGAACCATTAAGCTTTGGCTGTATCAGACC 240
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QY 361 GCCCATGCCAGCCCTTAATGTCGCCGTGACATGATTAAGCAAGTACATTAATTTACT 420
DB 2118 GCCCATGCCAGCCCTTAATGTCGCCGTGACATGATTAAGCAAGTACATTAATTTACT 2177
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DB 2358 AGTAATTACCAATCATTTTACAACACTGTGTACATGTGAGGCTGC 2402

RESULT 6
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LOCUS AR482081 9335 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 19 from patent US 6699984.
ACCESSION AR482081
VERSION AR482081.1 GI:47244049
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9335)
AUTHORS Ainley, M., Amerstrong, K., Belmar, S., Folker, O., Hopkins, N.,
Menke, M.A., Paraddy, D., Petolino, J.F., Smith, K. and Woosley, A.
TITLE Regulatory sequences for transgenic plants
JOURNAL Patent: US 6699984-A 19 02-MAR-2004;
Dow Agrosciences LLC, Indianapolis, IN

FEATURES Location/Qualifiers
source 1..9335
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ORIGIN

Query Match 100.0%; Score 645; DB 6; Length 9335;
Best Local Similarity 100.0%; Pred. No. 7,8e-134;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAGAGTTCAATTCGCTTCCCTGCTGTTATGTTCTTATATTCATGCTCTGCAAAAGCT 60
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QY 61 ATAAAGTTGATCTGCAATATATTAACAAGTTAGTACACAAAGTTTGTACTTCAAG 120
DB 1818 ATAAAGTTGATCTGCAATATATTAACAAGTTAGTACACAAAGTTTGTACTTCAAG 1877
QY 121 TCTTTTAACTATATGTTGGTGCATTAATGAGTAATCCATATGAAAGTTGCAAG 180
DB 1878 TCTTTTAACTATATGTTGGTGCATTAATGAGTAATCCATATGAAAGTTGCAAG 1937
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DB 2238 ATGTTTACTTAACCTTAAGTGGCAATGATGAGCTCTGACGCAAGCAATGCTCTGT 2297
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QY 601 AGTAATTACCAATCATTTTACAACACTGTGTACATGTGAGGCTGC 645
DB 2358 AGTAATTACCAATCATTTTACAACACTGTGTACATGTGAGGCTGC 2402

RESULT 7
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LOCUS AX655393 2000 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 5263 from Patent WO03000898.
ACCESSION AX655393
VERSION AX655393.1 GI:29158207
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE 1
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Qian, S., Tao, Y., Whitman, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 5263 03-JAN-2003;
Syngenta Participations AG (CH)


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Query Match 7.1%; Score 45.8; DB 2; Length 12028;
Best Local Similarity 46.4%; Pred. No. 3.2;
Matches 149; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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1530 AATTAAATTTATGAGAAATCTGAGAAATTAATGTTATTAATTAATTAAT 1589
71 ATATCGCATATTAATTAACAAGTTAGCTACACAAGTTTGTACTCAAGCTTTAACT 130
1590 ATATATATATATATATATATATATATATATATTAAGAACTTTATTTATGATATTAAT 1649
131 ATATGTTGGTCAATTAAGATTATGAGTAAATCCATATGAAGTGTGCAAGAACTGAA 190
1650 ATAAAGTTCCCAATTGATATTAATTTGTGAACCTATTAATCTTTACAAAATAATGCAA 1709
191 AGGCAAAATTAACGAGTAACCCATTACTAGCTTGGCTGTATCAGACCAATTAAGTTGA 250
1710 AAAAATTAATATGAGGAAATATATATTAATGAAATATATGTAATTAAGATACATATATATA 1769
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311 TTTTGCTAACTCTTTAGTT 331
1830 GATTATTTGATATTTTGT 1850
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RESULT 9
AE001374 13383 bp DNA linear INV 04-OCT-2002
LOCUS
DEFINITION Plasmidium falciiparum 3D7 chromosome 2 section 11 of 73 of the
complete sequence.
ACCESSION AE001374 AE001362
VERSION AE001374.1 GI:3845100
KEYWORDS
SOURCE Plasmidium falciiparum 3D7
ORGANISM Plasmidium falciiparum 3D7
REFERENCE Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
1 (bases 1 to 13383)

AUTHORS	Gardner,M.J., Tetteijn,H., Carucci,D.J., Cummings,L.M., Aravind,L., Koonin,E.V., Shallow,S., Mason,T., Yu,K., Fujii,C., Pedersen,J., Shen,K., Jing,J., Aston,C., Lai,Z., Schwartz,D.C., Perera,M., Balzberg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Adams,M.D., Venter,J.C. and Hoffman,S.L. Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum
JOURNAL	Science 282 (5391), 1126-1132 (1998)
PubMed	9804551
REFERENCE	2 (bases 1 to 13383)
AUTHORS	Gardner,M.J., Hall,N., Pung,B., White,O., Berriman,M., Hyman,R.W., Carlton,J.M., Pain,A., Nelson,K.E., Bowman,S., Paulsen,I.T., James,K., Eisen,J.A., Rutherford,K., Salzberg,S.L., Craig,A., Kyes,S., Chan,M.-S., Nene,V., Shallow,S.J., Suh,B., Peterson,J., Angiuoli,S., Pertea,M., Allen,J., Selengut,J., Haft,D., Mather,M.W., Valdivia,A.B., Martin,D.M.A., Falkland,A.H., Fraunholz,M.J., Roos,D.S., Ralph,S.A., McPadden,G.I., Cummings,L.M., Subramanian,G.M., Mungall,C., Venter,J.C., Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and Barrall,B.
TITLE	Genome sequence of the human malaria parasite Plasmodium falciparum
JOURNAL	Nature 419, 498-511 (2002)
REFERENCE	3 (bases 1 to 13383)
AUTHORS	Gardner,M.J.
TITLE	Direct Submission
JOURNAL	Submitted (02-OCT-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
FEATURES	Location/Qualifiers
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Db	3507	TTATATTTTATTTTATTTTAAATCCCATATTCAGATATATACAAATTTTGA--TTCA	3563	
Qy	79	GATATAATTAACAAGTTAGCTACACAAATTTTGTACTTCAAGTCTTTAACTATATGTTG	138	
Db	3564	GAATTAATTTTAATTTTCTCTTCAATATTTTAACTATATATTTTAAATTAATATTA	3623	
Qy	139	GTGCAATAGATTATGAGTAATCCATATGAAAGTGTGCAAGACATGAAG	192	
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LOCUS	BX510935	128666 bp	DNA	linear VRT 25-JUL-2005
DEFINITION	Zebrafish DNA sequence from clone DK51-207124 in linkage group 14,			
ACCESSION	BX510935			
VERSION	BX510935.28	GI:71142384		
KEYWORDS	HTG.			
SOURCE	Danio rerio (zebrafish)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Actinopterygii, Neopterygii, Teleostei, Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 128666)
Chapman, J.
Direct Submission
Submitted (23-JUL-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests:
http://www.sanger.ac.uk/Projects/Danio/facts.shtml#details
On Jul 25, 2005 this sequence version replaced gi:62719232.
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Center: Wellcome Trust Sanger Institute
Genome Center
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C.elegans/wormpep
Clone-derived Zebrafish pUC subclones occasionally display
inconsistency over the length of mononucleotide A/T runs and
conserved TA repeats. Where this is found the longest good quality
representation will be submitted.
Any regions longer than 1kb tagged as misc-feature 'unsure' are
part of a tandem repeat of more than 10kb in length where it has
not been possible to anchor the base differences between repeat
copies. The region has been built up based on the repeat element
to match the total size of repeat indicated by restriction digest,
but repeat copies may not be in the correct order and the usual
finishing criteria may not apply.
DKEY-207L24 is from a Zebrafish BAC library
VECTOR: pIndigoBAC-5.
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Best Local Similarity 49.6%; Pred. No. 3.4;
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72395 ATTTTCATTTCAAGTATAGTTCAATGTTGCTCTTTAGAAATTAATAA 72346

RESULT 11

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CO869722/c
LOCUS CO869722 138363 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 143 from Patent WO2004074320.
ACCESSION CO869722
VERSION CO869722.1 GI:51999546
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Morris, D.W., Morris, D.W. and Majandro, M.S.
AUTHORS Novel therapeutic targets in cancer
TITLE Patent: WO 2004074320-A 143 02-SEP-2004;
JOURNAL Sages Discovery, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 53.1%; Pred. No. 4.6;
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LOCUS AL157402/c
DEFINITION 210331 bp DNA linear PRI 18-MAY-2005
Human DNA sequence from clone RP11-553K8 on chromosome 1q31.2-31.3
Concerns the ATP6V1G3 gene for H+ transporting ATPase lysosomal
13kDa VI subunit G isoform 3, two novel genes, a prostatic binding
protein (PBP) pseudogene and the 5' end of the PTPRC gene for
receptor type protein tyrosine phosphatase C, complete sequence.
ACCESSION AL157402
VERSION AL157402.1 GI:13398702
KEYWORDS HTG; ATP6V1G3; PBP; PTPRC.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 210331)
Davidson, C.
Direct Submision
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequests@sanger.ac.uk
On Mar 21, 2001 this sequence version replaced gi:12717935.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-553K8 is from the library RPCI-11.2 constructed by the group

of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone, and the assembly was confirmed by restriction digest,
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FEATURES
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THORS	Taylor,C.A. and Knouft,J.H.				
RE	Historical influences on genital morphology among sympatric				
TTLE	crayfishes: systematics and gonopod evolution in the genus				
	Oronectes (Cambaridae)				
JURNAL	Unpublished				
RENCE	2 (bases 1 to 1525)				
THORS	Taylor,C.A. and Knouft,J.H.				
TTLE	Direct Submission				
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Best Local Similarity 45.9%; Pred. No. 6.7;

Matches 146; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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Db	10834	AAGTTATATATATTTTCAT 10817	

Search completed: February 11, 2006, 23:44:43
Job time : 3916 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:25:29 ; Search time 556 Seconds

(Without alignments)
7731.523 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645
Sequence: 1 GTCAGAGCTTCATTCCTT.....TGTTCATGCTAGGCGTGC 645

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	645	100.0	1682	12	ADJ48190	Adj48190 Maize oil
2	645	100.0	6550	2	AAV63737	AAV63737 Maize per
3	645	100.0	9335	2	AAV63737	AAV63737 Maize per
4	557	86.4	709	12	ADJ48004	Adj48004 Maize oil
5	47.6	7.4	1119	12	ADJ48213	Adj48213 Maize oil
6	47.6	7.4	2000	11	ACU35363	ACU35363 Rice stre
7	46.2	7.2	2000	8	ADA71938	Ada71938 Rice gene
8	43.8	6.8	138163	13	ABD32624	ABD32624 Human can
9	42.8	6.6	2000	11	ACU35363	ACU35363 Rice stre
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11	40.2	6.2	10710	6	ABL32893	ABL32893 Human imm
12	40.2	6.2	19459	6	ABK31213	ABK31213 Signal tr
13	40.2	6.2	19459	6	ABL70528	ABL70528 Chemical
14	40.2	6.2	33053	6	ABO67006	ABO67006 Human ang
15	40.2	6.2	40862	6	ABL34072	ABL34072 Human imm
16	39.6	6.1	2000	8	ADA71938	Ada71938 Rice gene
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18	39.4	6.1	83391	6	ABO67093	ABO67093 Human ang
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C	20	39.2	6.1	3531	12	ADG63920	Adg63920 Novel hum
C	21	39.2	6.1	4782	8	ACC44434	Acc44434 Gene enco
C	22	39.2	6.1	5052	12	ADG64457	Adg64457 Novel hum
C	23	39.2	6.1	6145	12	ADG22133	Adg22133 Human so
C	24	39.2	6.1	8757	10	ADG29766	Adg29766 Human tum
C	25	38.8	6.0	7134	6	ABL32483	AbL32483 Human imm
C	26	38.8	6.0	10467	6	ABK28454	AbK28454 DNA trans
C	27	38.6	6.0	5930	6	ABL32517	AbL32517 Human imm
C	28	38.6	6.0	7108	6	ABK39996	AbK39996 Human che
C	29	38.6	6.0	9905	6	ABL32062	AbL32062 Human imm
C	30	38.6	6.0	10329	6	ABL34122	AbL34122 Human imm
C	31	38.6	6.0	10886	6	ABL34134	AbL34134 Human imm
C	32	38.6	6.0	13511	6	ABL32281	AbL32281 Human imm
C	33	38.6	6.0	18512	6	ABL32977	AbL32977 Human imm
C	34	38.2	5.9	19577	6	ABL33420	AbL33420 Human imm
C	35	37.6	5.8	2000	11	ACU37108	ACU37108 Rice stre
C	36	37.6	5.8	38596	10	ADG63503	Adg63503 Mycoplaem
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C	41	37.2	5.8	567	14	ADV74973	Adv74973 Human col
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C	44	37.2	5.8	1726	9	ACH04267	Ach04267 Human CDN
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ALIGNMENTS

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AC	ADJ48190;	
XX	DT	06-MAY-2004 (first entry)
XX	DE	Maize oil-associated gene #8.
XX	KW	de; maize; plant; oil-associated gene; transgenic; enhanced seed oil;
XX	KM	vegetable oil.
XX	OS	Zea mays.
XX	XX	
XX	PN	US2004025202-A1.
XX	PD	05-FEB-2004.
XX	PF	14-MAR-2003; 2003US-00389566.
XX	PR	15-MAR-2002; 2002US-0365301P.
XX	PR	26-JUN-2002; 2002US-0391786P.
XX	PR	26-JUN-2002; 2002US-0392018P.
XX	PA	(LAUR/ LAURIE C C.
XX	PA	(RAVA/ RAVANELLO M.
XX	PA	(SAVA/ SAVAGE T.
XX	PA	(LEDE/ LEDEAUX J R.
XX	PA	(ROGE/ ROGERS J A.
XX	PI	Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX	XX	
XX	DR	WPI; 2004-142683/14.
XX	PT	Novel recombinant DNA construct comprising a promoter functional in
XX	PT	plants operably linked to an oil-associated gene for producing transgenic
XX	PT	plant seed.
XX	XX	Example 1; SEQ ID NO 194; 22pp; English.
XX	XX	The invention relates to a recombinant DNA construct comprising a

CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents a maize oil-
CC associated gene.

XX Sequence 1682 BP; 426 A; 398 C; 379 G; 479 T; 0 U; 0 Other;

Query Match 100.0%; Score 645; DB 12; Length 1682;
Best Local Similarity 100.0%; Pred. No. 1.3e-166;

Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 379 ATAAAGCTGATCTGAGATATATATATATACAGTTAGCTACAGAGTTTGACTTCAAG 438
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QY 421 CTATGTTCTCCTTTTGTAGTGTCTGTATAGATGTCCTTTTGTGAGCCATCGAGAG 480
    |||
DB 739 CTATGTTCTCCTTTTGTAGTGTCTGTATAGATGTCCTTTTGTGAGCCATCGAGAG 798
    |||
QY 481 ATGTTTACTTAATCTTATGTCGCAATGATGAGAGCTCTCAGTGCACGCAATGCTCTGT 540
    |||
DB 799 ATGTTTACTTAATCTTATGTCGCAATGATGAGAGCTCTCAGTGCACGCAATGCTCTGT 858
    |||
QY 541 AATCTACTGTCAACACATCTGTATGTCGCTTAATCTTAATCTTAATCTTAATCTTAATCT 600
    |||
DB 859 AATCTACTGTCAACACATCTGTATGTCGCTTAATCTTAATCTTAATCTTAATCTTAATCT 918
    |||
QY 601 AGTATATTACCAATCATTTACACACTGTATCATGTAGAGGCTGC 645
    |||
DB 919 AGTATATTACCAATCATTTACACACTGTATCATGTAGAGGCTGC 963
    |||
```

RESULT 2

AAV63717

AAV63717 standard; DNA; 6550 BP.

XX AAV63717;

XX 12-APR-1999 (first entry)

XX Malze per5 root preferential cationic peroxidase gene.

KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds.

OS Zea mays.

```
XX Key
FH promoter
FT Location/Qualifiers
    1..4215
    /tag= a
    /note= "this region is specifically claimed in Claim 1"
    1..4200
    /tag= c
    /note= "this region is specifically claimed in Claim 1"
    1..4148
    /tag= b
    /note= "this region is specifically claimed in Claim 1"
    2532..4215
    /tag= f
    /note= "this region is specifically claimed in Claim 1"
    2532..4200
    /tag= e
    /note= "this region is specifically claimed in Claim 1"
    2532..4148
    /tag= d
    /note= "this region is specifically claimed in Claim 1"
    3187..4215
    /tag= i
    /note= "this region is specifically claimed in Claim 1"
    3187..4200
    /tag= h
    /note= "this region is specifically claimed in Claim 1"
    3187..4148
    /tag= g
    /note= "this region is specifically claimed in Claim 1"
    4086..4215
    /tag= j
    /note= "this region is specifically claimed in Claim 1"
    4086..4200
    /tag= k
    /note= "this region is specifically claimed in Claim 1"
    4086..4148
    /tag= l
    /note= "this region is specifically claimed in Claim 1"
    4201..6068
    /tag= m
    /note= "this region is specifically claimed in Claim 1"
    4201..4425
    /tag= n
    /note= "this region is specifically claimed in Claim 1"
    4420..5064
    /tag= o
    /note= "this region is specifically claimed in Claim 2"
    4426..5058
    /tag= p
    /note= "this region is specifically claimed in Claim 2"
    5059..5250
    /tag= q
    /note= "this region is specifically claimed in Claim 2"
    5245..5388
    /tag= r
    /note= "this region is specifically claimed in Claim 2"
    5251..5382
    /tag= s
    /note= "this region is specifically claimed in Claim 2"
    5383..5548
    /tag= t
    /note= "this region is specifically claimed in Claim 2"
    5542..5654
    /tag= u
    /note= "this region is specifically claimed in Claim 2"
    5542..5654
    /tag= v
    /note= "this region is specifically claimed in Claim 2"
    5549..5649
    /tag= v
```


FT /number= 3
FT /note= "this intron is specifically claimed in Claim 2"
FT exon /tag= w
FT /number= 4
FT 3' UTR /tag= y
FT /note= "transcription termination sequence, specifically
FT claimed in Claim 3"
XX
XX MO9856921-A1.
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98MO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (IDMC) DOW AGROSCIENCES LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
XX Pareddy D, Pecolino JF, Smith K, Woosley A;
XX MPI; 1999-080904/07.
XX P-PSDB; AAW87893.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX PT derived from the maize root preferential cationic peroxidase protein
XX PT (pers) gene.
XX
XX Claim 1; Page 84-89; 150pp; English.
XX
XX This is the nucleotide sequence of the maize pers root preferential
XX CC cationic peroxidase gene, which encodes a 333-amino acid peroxidase
XX CC polypeptide (see AAW87893). Genomic clones comprising pers sequences were
XX CC isolated from a maize W22 genomic library using a probe based on isolated
XX CC pers cDNA. Overlapping subfragments of the gene were sequenced to
XX CC determine the complete 6550 bp sequence of the pers gene. Regulatory
XX CC sequences derived from the pers gene, including the promoter, introns and
XX CC 3' untranslated region (3' UTR), are used in claimed recombinant gene
XX CC cassettes for controlling expression of recombinant genes in selected
XX CC tissue, especially the root, of transformed plants, particularly maize.
XX CC The gene cassettes can be used for expression of heterologous genes such
XX CC as those that confer tolerance to herbicides, insects or viruses, and
XX CC genes that provide improved nutritional value or processing
XX CC characteristics to the plant. Use of the pers 3' UTR sequences provides
XX CC enhanced expression compared to similar gene cassettes utilizing the nos
XX CC 3' UTR
XX
XX Sequence 6550 BP; 1844 A; 1427 C; 1346 G; 1933 T; 0 U; 0 Other;
SQ

Db 4660 AATAACTGGAATGCACTTGCTGACATGCTCTAAGATTTAGAAAAGGTAGACGGAGA 4719
Qy 301 ATCTAATATTTTGGCTAATCTTTAGTACTATTTGATTTGATGAGAAAGCCATCACTT 360
Db 4720 ATCTAATATTTTGGCTAATCTTTAGTACTATTTGATTTGATGAGAAAGCCATCACTT 4779
Qy 361 GCCATGCCAGCCCTAATGTCGCCGATGACATGATGAGCCAGTACTATTAATTTACT 420
Db 4780 GCCATGCCAGCCCTAATGTCGCCGATGACATGATGAGCCAGTACTATTAATTTACT 4839
Qy 421 CTATGTTCTCTTTTGAAGTCGTATTAAGATGTCCTTTTGAAGCCACTGAGAAAG 480
Db 4840 CTATGTTCTCTTTTGAAGTCGTATTAAGATGTCCTTTTGAAGCCACTGAGAAAG 4899
Qy 481 ATGTTAATTAATCTAATGAGCGAATGATTTGAGCTCTCATGTCAGCATGTGCTCTGT 540
Db 4900 ATGTTAATTAATCTAATGAGCGAATGATTTGAGCTCTCATGTCAGCATGTGCTCTGT 4959
Qy 541 AATCTAATGTCAGCACTACTCTGATGATGTCCTTAACTCTAATCTATTGCACTGAGCT 600
Db 4960 AATCTAATGTCAGCACTACTCTGATGATGTCCTTAACTCTAATCTATTGCACTGAGCT 5019
Qy 601 AGTAATTAATCAATCTTACACACCTGTATCATGTGTAGGGCTGC 645
Db 5020 AGTAATTAATCAATCTTACACACCTGTATCATGTGTAGGGCTGC 5064

RESULT 3
AAV63734
ID AAV63734 standard; DNA; 9335 BP.
XX
XX AAV63734;
AC
XX 12-APR-1999 (first entry)
XX
XX DB Plasmid pIGP/367 containing the pers promoter and Intron 1.
XX
XX KM Peroxidase; pers gene; maize; corn; transgenic plant; promoter; root;
XX vector; plasmid pIGP/367; ds; circular; cyclic.
XX
XX OS Escherichia coli.
XX OS Zea mays.
XX OS Zea mays subsp. mays; streak virus.
XX OS Agrobacterium tumefaciens.
XX OS Cauliflower mosaic virus.
XX OS Synthetic.
XX OS Chimeric.
XX
XX
XX Key Location/Qualifiers
FT misc_feature 1..40
FT /tag= a
FT /note= "synthetic polylinker"
FT misc_feature 41..75
FT /tag= b
FT /note= "pCR2.1 polylinker"
FT promoter 81..1741
FT /tag= c
FT /note= "pers promoter nt 2532-4192"
FT exon 1748..1763
FT /tag= d
FT /note= "pers exon 1"
FT intron 1764..2396
FT /tag= e
FT /note= "pers intron 1"
FT exon 2397..2405
FT /tag= f
FT /note= "pers exon 2"
FT CDS 2408..4215
FT /tag= g
FT /product= "beta-glucuronidase"
FT /note= "GUS gene"
FT 4217..4264
FT /tag= h
FT misc_feature

```
FT /note= "sequence from PB1221"
FT 4280..4652
FT /*tag= 1
FT /note= "pers 3'UTR"
FT 4653..4869
FT /*tag= 3
FT /note= "synthetic linker"
FT 4870..5121
FT /*tag= k
FT /note= "CamV DNA nt 7093-7344"
FT 5122..5129
FT /*tag= 1
FT /note= "linker"
FT 5130..5476
FT /*tag= m
FT /note= "CamV DNA nt 7093-7439"
FT 5477..5496
FT /*tag= n
FT /note= "linker"
FT 5497..5606
FT /*tag= o
FT /note= "maize streak virus synthetic leader (MSV nt 167-186, 188-277)"
FT 5608..5698
FT /*tag= p
FT /note= "Adh1.S nt 119-209"
FT 5699..5820
FT /*tag= q
FT /note= "Adh1.S nt 555-672 plus 4-base linker"
FT 5828..5864
FT /*tag= r
FT /note= "maize streak virus nt 278-317"
FT 5865..6419
FT /*tag= s
FT /product= "phosphinothricin acetyltransferase gene"
FT /note= "Basta resistance selectable marker"
FT 6420..6699
FT /*tag= t
FT /note= "nos 3'UTR"
FT 6700..9335
FT /*tag= u
FT /note= "pUC19 sequences"
XX
XX MO9856921-A1.
XX
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98MO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (DOWC ) DOW AGRSCIENCES LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA,
XX Pareddy D, Petolino JF, Smith K, Woosley A;
XX
XX WPI; 1999-080904/07.
XX
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (pers) gene.
XX
XX Example 17; Page 117-122; 150pp; English.
XX
XX This is the nucleotide sequence of PIGP/367, a plasmid containing the
XX maize root preferential cationic peroxidase pers gene (see (see AAV63717)
XX promoter, the pers untranslated leader modified to include the pers intron
XX 1, the GUS gene, and the pers 3' untranslated region (3'UTR). Because
XX intron flanking sequences (exon DNA) are important in the processing of
XX the intron, 16 bases of flanking exon DNA were included in the fusion
XX within the pers untranslated leader. Transformation experiments in maize
XX demonstrated that the presence of the pers intron is essential for root-
XX specific expression from the pers promoter. The invention relates to
```

```
CC Isolated regulatory sequences, especially promoter, intron and 3'UTR
CC sequences, of the maize pers gene. Claimed recombinant gene cassettes
CC comprising pers regulatory sequences are used to control expression of
CC recombinant genes in selected tissue, especially the root, of transformed
CC plants, particularly maize
XX
SQ Sequence 9335 BP; 2402 A; 2290 C; 2258 G; 2385 T; 0 U; 0 Other;
Query Match 100.0%; Score 645; DB 2; Length 9335;
Best Local Similarity 100.0%; Pred. No. 2,3e-166;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCAAGGTCGAATTCGCTTCCTCTGTTATGTTCTTATATTAACATGCTCTGCAAAAGCT 60
DB 1758 GTCAAGGTCGAATTCGCTTCCTCTGTTATGTTCTTATATTAACATGCTCTGCAAAAGCT 1817
QY 61 ATTAAGCTTGATACGCACTATTAATTAACAAGTTGCTACACAACTTTTGTACTCAAG 120
DB 1818 ATTAAGCTTGATACGCACTATTAATTAACAAGTTGCTACACAACTTTTGTACTCAAG 1877
QY 121 TCTTTTAACTATATGTTGGTGCAATTAAGATTATGAATTAATCAATGAAGTGTGCAAG 180
DB 1878 TCTTTTAACTATATGTTGGTGCAATTAAGATTATGAATTAATCAATGAAGTGTGCAAG 1937
QY 181 AGAACAATGAAGCAAAAGATTAACGAGATGAACCACTTACTAGCTTGGCTGTATCAAGCC 240
DB 1938 AGAACAATGAAGCAAAAGATTAACGAGATGAACCACTTACTAGCTTGGCTGTATCAAGCC 1997
QY 241 AATAACTTGAATATGCACTGTGTGTAACATGCCATTAATTAAGAAAGCTTGAGAGA 360
DB 1998 AATAACTTGAATATGCACTGTGTGTAACATGCCATTAATTAAGAAAGCTTGAGAGA 2057
QY 301 ATCTATATATTTTGGCTAACTCTTTAGTACTATTTGATTGATGAGAAAGCTTACCAT 360
DB 2058 ATCTATATATTTTGGCTAACTCTTTAGTACTATTTGATTGATGAGAAAGCTTACCAT 2117
QY 361 GCCCATGCAAGCCCTAATGTCGCCGTGACATGATGAGCCAGTACTATGATTAATTTACT 420
DB 2118 GCCCATGCAAGCCCTAATGTCGCCGTGACATGATGAGCCAGTACTATGATTAATTTACT 2177
QY 421 CTAATGTCCTCCCTTTTGAAGTCGTATTAAGATGTCCTTTTGAAGCCAGTCAAGAG 480
DB 2178 CTAATGTCCTCCCTTTTGAAGTCGTATTAAGATGTCCTTTTGAAGCCAGTCAAGAG 2237
QY 481 ATGTTACTTAATCTAGTGGCAATGATGAGCTCTGAGTCAACGCAATGCTCTGT 540
DB 2238 ATGTTACTTAATCTAGTGGCAATGATGAGCTCTGAGTCAACGCAATGCTCTGT 2297
QY 541 AATCTACTGTCACCACTACTCTGTAGTGTGTGCTTAACCTTAACCTATTTCCAGTGGCT 600
DB 2298 AATCTACTGTCACCACTACTCTGTAGTGTGTGCTTAACCTTAACCTATTTCCAGTGGCT 2357
QY 601 AGTAATTACCAATCACTTCAACACGTGTACAGTGAAGGCGTCG 645
DB 2358 AGTAATTACCAATCACTTCAACACGTGTACAGTGAAGGCGTCG 2402
RESULT 4
ADJ48004
ID ADJ48004 standard; DNA; 709 BP.
XX
XX ADJ48004;
XX
XX 06-MAY-2004 (first entry)
XX
XX Maize oil-associated gene genomic amplicon #8.
XX
XX de; maize; plant; oil-associated gene; transgenic; enhanced seed oil;
XX vegetable oil.
XX
XX Zea mays.
XX
XX US2004025202-A1.
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XX 05-FEB-2004.
PD 14-MAR-2003; 2003US-00389566.
XX 15-MAR-2002; 2002US-0365301P.
XX 26-JUN-2002; 2002US-0391786P.
XX 26-JUN-2002; 2002US-0392018P.
XX (LAUR/) LAURIE C. C.
XX (RAVA/) RAVANELLO M.
XX (SAVA/) SAVAGE T.
XX (LEDE/) LEDEAUX J. R.
XX (ROGE/) ROGERS J. A.
XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX Example 1; SEQ ID NO 8; 22pp; English.
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents a maize oil-
XX associated gene genomic amplicon.
XX Sequence 709 BP; 203 A; 141 C; 155 G; 210 T; 0 U; 0 Other;
XX
XX Query Match 86.4%; Score 557; DB 12; Length 709;
XX Best Local Similarity 99.1%; Pred. No. 1.4e-142;
XX Matches 560; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 81 ATATATTAACAAGTCTAGTACACAGTTTGTACTTCAAGTCTTTTAACTATATGTTGT 140
XX 1 ACATATTAACAAGTCTAGTACACAGTTTGTACTTCAAGTCTTTTAACTATATGTTGT 60
XX 141 GCATTAAGATTATGAGTAATCCATATGAGTGTGCAAGCAATATGAAAGCAAGAT 200
XX 61 GCATTAAGATTATGAGTAATCCATATGAGTGTGCAAGCAATATGAAAGCAAGAT 120
XX 201 AAACGATGAACCCATTACTAGCTTGGCTGTATCAAGCAATTAATCTTGAATGCACTTG 260
XX 121 AAACGATGAACCCATTACTAGCTTGGCTGTATCAAGCAATTAATCTTGAATGCACTTG 180
XX 261 TGTCTAGCATCTTAAGTATTAAGAAAGGTAGCATGGGGAATCTATATTTTGGCTAA 320
XX 181 TGTCTAGCATCTTAAGTATTAAGAAAGGTAGCATGGGGAATCTATATTTTGGCTAA 240
XX 321 GTTCTTAACTATTAATGATTAAGAAAGGTAGCATGGGGAATCTATATTTTGGCTAA 380
XX 241 GTTCTTAACTATTAATGATTAAGAAAGGTAGCATGGGGAATCTATATTTTGGCTAA 300
XX 381 CCCGGTGAACATTAATGATTAAGAAAGGTAGCATGGGGAATCTATATTTTGGCTAA 440
XX 301 CCCGGTGAACATTAATGATTAAGAAAGGTAGCATGGGGAATCTATATTTTGGCTAA 360
XX 441 GTCTGTATTAAGATGCTCTTTTGGCACTCGAAGAAATGTTTAACTTAAGTCTAGT 500
XX 361 GTCTGTATTAAGATGCTCTTTTGGCACTCGAAGAAATGTTTAACTTAAGTCTAGT 420
XX 501 CGCAATGATTGAGCTCTGAGTGAAGCAAGCATGCTCTGTAATCTAAGTCAACCACTACT 560
XX 421 CGCAATGATTGAGCTCTGAGTGAAGCAAGCATGCTCTGTAATCTAAGTCAACCACTACC 480

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XX 561 CTGTAGTGTGCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAAC 620
XX 481 CTGTAGTGTGCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAAC 540
XX 621 AACCTGTTAATCAATGTTAGGCTGC 645
XX 541 AACCTGTTAATCAATGTTAGGCTGC 565
XX
XX RESULT 5
XX ADJ48213
XX ID ADJ48213 standard; DNA; 1119 BP.
XX ADJ48213;
XX AC ADJ48213;
XX DT 06-MAY-2004 (first entry)
XX DE Maize oil-associated gene #31.
XX XX de; maize; plant; oil-associated gene; transgenic; enhanced seed oil;
XX KW vegetable oil.
XX OS Zea mays.
XX PN US2004025202-A1.
XX PD 05-FEB-2004.
XX PF 14-MAR-2003; 2003US-00389566.
XX PR 15-MAR-2002; 2002US-0365301P.
XX PR 26-JUN-2002; 2002US-0391786P.
XX PR 26-JUN-2002; 2002US-0392018P.
XX XX (LAUR/) LAURIE C. C.
XX PA (RAVA/) RAVANELLO M.
XX PA (SAVA/) SAVAGE T.
XX PA (LEDE/) LEDEAUX J. R.
XX PA (ROGE/) ROGERS J. A.
XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX Example 1; SEQ ID NO 217; 22pp; English.
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents a maize oil-
XX associated gene.
XX Sequence 1119 BP; 279 A; 283 C; 265 G; 292 T; 0 U; 0 Other;
XX
XX Query Match 7.4%; Score 47.6; DB 12; Length 1119;
XX Best Local Similarity 85.5%; Pred. No. 0.011;
XX Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX 584 AACTATTCACGCGGTAGTAATTAACATTAATTAACATTAATTAACATTAATTAAGGCT 643
XX 15 AACAGTTAGCGACACAGTAATTAACATTAATTAACATTAATTAAGGCT 74
XX 644 GC 645
XX 75 GC 76
XX

```

```
RESULT 6
ACLS35363/C
ID ACL35363 standard, cDNA, 2000 BP.
XX
XX ACL35363,
AC
XX
XX 02-JUN-2005 (first entry)
DT
XX
XX Rice stress-regulated promoter SEQ ID NO:13926.
DE
XX
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KM agriculture.
XX
XX Oryza sativa.
OS
XX
XX WO2003008540-A2.
PN
XX
XX 30-JAN-2003.
PD
XX
XX 21-JUN-2002; 2002MO-US019668.
PF
XX
XX 22-JUN-2001; 2001US-0300112P.
PR
XX 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN ) SYNGENRA PARTICIPATIONS AG.
XX
XX Krepes J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
PI Moughamer T, Provart N, Rieke D, Zhu T,
XX
XX WPI; 2003-248011/24.
DR
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX
XX Claim 48; SEQ ID NO 13926; 899p; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX
XX Sequence 2000 BP; 540 A; 344 C; 416 G; 428 T; 0 U; 272 Other;
SQ
Query Match 7.4%; Score 47.6; DB 11; Length 2000;
Best Local Similarity 15.6%; Pred. No. 0.013;
Matches 56; Conservative 145; Mismatches 159; Indels 0; Gaps 0;
OY 104 AAGTTTGTAAGTCTTCAAGTCTTAACTATATGTTGGCAATAGATTATGATATCA 163
DB 369 AAGTCGTTTASGCMWKTMMKTMMKTKKAAKAAKAAWYVMSRYRMYYSW 310
OY 164 TATGAAAGCTTTGCAAGAAACATGAAAGCAAAAGATAAACGATGAACCCATTATGAC 223
DB 309 AAWAGSWRWSKTBARBSWNAWKTKWAKWYBAVSKWKKKKWYWTBAAMWATMTMM 250
OY 224 TTTCGGCTGTATCAGACCAATTAATTGAAATGCACTTGTGCTGATGATGCTTAAGATTA 283
DB 249 TMMWRKWTBYMAKWTYAAWMTYAAWAAWTAATATMTKATRGAAWMTWSWAGWAAAKWY 190
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OY 284 AAAGTAGCATGAGAGAAATCTATATTATTTGGCTAACTCTTAACTATGATTA 343
DB 189 WTKRYWTRBARAGMYRRTMKMTSMCTMMWMMWMTTWTYRKAARAKARAGATW 130
OY 344 TGAAGAAAGCTTACCATTCGCCATGCGCCCTTAATGTCGGGTGACATGATTAGCAGT 403
DB 129 WWRKYAMSWTWTKRKYMMKRTMRWKYCCRAAMWSWCTKSWWWWYKSTWSKMSGS 70
OY 404 ACTATGATTAATTATCTATATTGTTCTCGTTTGTAGTGTGATTAAGATGCTTTT 463
DB 69 AGTMTKYAKYMMWTRKTRKTRISWKAAMTCCNRKATCMKMMKMMYKTYT 10

RESULT 7
ADA71938/C
ID ADA71938 standard, DNA; 2000 BP.
XX
XX ADA71938;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Rice gene, SEQ ID 5263.
DE
XX
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KM gene; ds.
XX
XX Oryza sativa.
OS
XX
XX WO2003000898-A1.
PN
XX
XX 03-JAN-2003.
PD
XX
XX 22-JUN-2001; 2001MO-IB001105.
PF
XX
XX 22-JUN-2001; 2001MO-IB001105.
PR
XX
XX (SYGN ) SYNGENRA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
DR
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX
XX Claim 27; SEQ ID NO 5263; 899p; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
XX
XX Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
SQ
Query Match 7.2%; Score 46.2; DB 8; Length 2000;
Best Local Similarity 12.2%; Pred. No. 0.031;
Matches 63; Conservative 225; Mismatches 218; Indels 11; Gaps 1;
OY 12 ATTCTGCTTCCTGTATGTTCTTATATTAATATGATGCTGCAAGCTATAAGCTTGA 71
DB 987 WKRYMAVKRYAMWSRKTWCTGKRATITGCTMMAGRRWRWAMCMYCCMMKMWK 928
OY 72 TACTGAGATTAATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAGTCTTTAACTA 131
```

Db 927 MTSCMWMKXVTRWSCVTTMMGABRYAVYAMRRBRMTYKMSNRMYTMTKMMATMTMCM 866
Qy 132 TATGTTGGTCAATTAAGTATGATGATATGAGTGTGTCAGAGAACATGAA 191
Db 867 CNAKMYATWATMMWRYTMYTCYAMTCAKCKYKNAATKMTTMACAWRATSWRRAM 808
Qy 192 GGCNAAGATAAGCGAGTACCCCATCTACTGCTTGCTGATGACCAATACTGAA 251
Db 807 AGRRMKRYKMKRAYWMMWMCWKAAGMARMKSRYRMKCKATRTYKMMATMMWRR 748
Qy 252 ATGCACTGTGCTAGCATGCTAGTATTAAGAAAGTAGACAGAGAACTATATTAT 311
Db 747 MKSYBMWSGMBRMSAMRYCSRMKCAKTYASABATKRAKSYRRRRMYW----- 695
Qy 312 TTTGGCTAACCTTTTGTGTTACTATGATGATGAGAAAGCTACCATGCGCCAG 371
Db 694 ----KRGMTYRYRYWRSCTMTBAMSKRRKRWAGASMSCMYWRGARSMWYSKYCSAK 639
Qy 372 CCCAATGTCGCGGTGACATGATGAGCCAGTACTATGATTAATTACTGTTCTC 431
Db 638 CCKKRTMTSYSTGMYTGYSTYSKMSMTSKMSYMGMTCTMTYSKSGSTRSKGRWS 579
Qy 432 CTTTGTGAGTGTGATTAAGATGCTCTTTTGTGAGCCACTCGAAGAGATGTTACTTA 491
Db 578 GMSRMVRYMKRKRKRYMYMKKCTWRKCMCYRWGYTMTTYSRSMYTTGRYKAYTS 519
Qy 492 ACTCTACTGCGCAATGATTTGAGAGCTCTCAGTCAAG 538
Db 518 KRRYMYKYRKYCYVYYGYMYKCSYMMRYGYCWACK 482

RESULT 8
ABD32624/c
ID ABD32624 standard; DNA; 138363 BP.
XX
AC ABD32624;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated genomic DNA HD13-011.
XX
KM Human; db; cancer-associated protein; gene; cytoskeletal; cancer;
XX
OS Leukemia; Lymphoma; CAP.
XX
PN Homo sapiens.
XX
PD W02004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
XX
PR 14-MAR-2003; 2003US-00388838.
XX
PR 15-APR-2003; 2003US-00417375.
XX
PR 13-JUN-2003; 2003US-00461862.
XX
PR 15-SEP-2003; 2003US-00663431.
XX
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS,
XX
DR WPI, 2004-652914/63.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
XX
PT for diagnosing, preventing or treating cancers, especially lymphoma and
XX
PT leukemia, or in screening for agents that modulate cancer.
XX
PS claim 16; seqid 143; 310pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising at least 10

CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Seq Sequence 138363 BP; 44034 A; 23484 C; 24178 G; 46647 T; 0 U; 20 Other;

XX Query Match 6.8%; Score 43.8; DB 13; Length 138363;

XX Best Local Similarity 53.1%; Pred. No. 0.55; Matches 93; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 37 TATATTACATGCTCTGACAAAGCTATTAAGCTTGATCTGAGATTAATTAACAAGTTA 96
Db 68785 TCTTGTACTTGTGCTGTGAGGACGACATGACATTTATTTAACTCTTATTCATTA 68726
Qy 97 GCTACCAAGTTTGTACTCTCAAGCTTTTAACTATATGTTGCAATAAGTTATGAG 156
Db 68725 ACTTCATCAGTAAGTAAAGTAAATCTTGATGTAACCTTAACAATTTCTGTGATGG 68666
Qy 157 TAATCATATGAAGTGTGCAAGAGACATGAAGGCAAGATTAACGATGAA 211
Db 68665 TATTATATATGCTTGTTTTCAACAGATTAATGATGTTTAAAGCTTCA 68611

RESULT 9
ACL35363
ID ACL35363 standard; cDNA; 2000 BP.
XX
AC ACL35363;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice stress-regulated promoter SEQ ID NO:13926.
XX
DE abiotic stress tolerance; transgenic plant; plant; cereal;
XX
OS agriculture.
XX
OS Oryza sativa.
XX
PN W02003008540-A2.
XX
PD 30-JUN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.

PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PI Krepes J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
PI Moughamer T, Provart N, Riecke D, Zhu T;
XX WPI; 2003-248011/24.
XX
PT New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
PS Claim 48; SEQ ID NO 13926; 89pp; English.
XX
CC The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 2000 BP; 540 A; 344 C; 416 G; 428 T; 0 U; 272 Other;
Query Match 6.6%; Score 42.8; DB 11; Length 2000;
Best Local Similarity 11.4%; Pred. No. 0.26; Mismatches 115; Indels 0; Gaps 0;
Matches 32; Conservative 133; Mismatches 115; Indels 0; Gaps 0;
QY 70 GATACGACGATATATATACCAAGTGTGCTACACAGCTTTGTACTTCAAGTCTTTTAAAC 129
DB 2 SMRSKKTAAAMARMMKMKMKMMKMGKAKAYYKGGAKMTWMSAYMAYMMYAKKKKRM 61
QY 130 TATATGTTGGTCATATAGATTAGTAAATCATATGAAAGTGTGCAAGAGAATCTATG 189
DB 62 TRNAKRCCTSCSKYMSAKRMWMSARMSKMTYGGRMWRKAYKAYMMKMMYMAWAM 121
QY 190 AAGCGAAAGATTAACGATGACCATTTACTAGCTTTGGCTGTACAGACCAATCTATG 249
DB 122 SMTMTMWWAKCTCYTMYKTMWYRMAAAWRMRKWKMMWARGMSAKMAYRRKRCY 181
QY 250 AATGACACTTGTCAGATGCTCTAAGATATTAGAAAAGTGAAGGAGATCTATATT 309
DB 182 YMAWRMAWRMTTTRKCTMSWYAMWTCTATMAATATTTTMMAMWKRATMTWRYA 241
QY 310 ATTTGGCTAACTTCTTGAATATTGATGATGATGAGAA 349
DB 242 WMYTMMWAKKWAAMKATKMTTYAWRMMWMMMSRTTYRM 281
RESULT 10
ABL55643/C
ID ABL55643 standard; DNA; 50000 BP.
XX
AC ABL55643;
XX
DT 01-JUL-2002 (first entry)
XX
DE AmEPV genome fragment#1.
XX
XX AmEPV, gene therapy; viral vector; chromosome mapping; gene mapping;
KW genetic deficiency disorder; ds.
XX
OS Amacta moorei entomopoxvirus.

XX
PN WO200212526-A2.
XX
PD 14-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US025287.
XX
PR 10-AUG-2000; 2000US-0224479P.
PR 14-SEP-2000; 2000US-00662254.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Moyer RM, Li Y, Bawden AL;
XX WPI; 2002-227161/28.
XX
PT Novel recombinant entomopox virus vector useful for delivering
PT polynucleotide encoding protein to vertebrate cell, comprises
PT polynucleotide encoding protein operably linked with heterologous
PT promoter sequence.
XX
PS Disclosure; Page 125-150; 326pp; English.
XX
CC The invention relates to a recombinant entomopox virus (EPV) vector,
CC comprising a polynucleotide encoding a protein operably linked with a
CC heterologous promoter sequence. The invention also concerns methods for
CC providing gene therapy for genetic deficiency disorders. Vectors of the
CC invention are useful for delivering a polynucleotide encoding a protein
CC to a vertebrate cell, preferably a mammalian cell, such as a human cell.
CC The vector is introduced into the vertebrate cell by infection in a viral
CC particle, or by transfection, transduction, or injection either in vitro
CC or in vivo. The vector is useful for the delivery and expression of
CC biologically useful proteins in gene therapy protocols, and for
CC delivering large DNA segments for engineering of vertebrate cells.
CC Polynucleotides of the invention have applications in techniques such as
CC their use as insertion sites for foreign genes of interest, hybridisation
CC probes, for chromosome and gene mapping, in PCR technologies, and in the
CC production of sense or antisense nucleic acids. Vectors of the invention
CC provide for stable integration and expression of heterologous DNA in host
CC cells, and are adapted for accepting large heterologous polynucleotide
CC inserts which can be delivered in an infected or transformed cell and
CC expressed in a stable fraction. The current sequence represents a
CC fragment of the genome of the genus B entomopoxvirus from amacta moorei
CC (AmEPV)
XX
SQ Sequence 50000 BP; 19857 A; 4373 C; 4222 G; 21548 T; 0 U; 0 Other;
Query Match 6.6%; Score 42.8; DB 6; Length 50000;
Best Local Similarity 45.9%; Pred. No. 0.75; Mismatches 172; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
QY 27 TTATGTTCTTATATTAACATGCTCTGACAAAGCTATTAAGCTTGATCTGACATATATA 86
DB 11134 TGAATTAATATGTAATTAATTAATTAATTTCTATTAAGATTAATTAATTAATTA 11075
QY 87 TAACAAGTTAGTCACCAAGTTTGTACTTCAAGCTTTTAACTATATGTTGGTCATA 146
DB 11074 TAAATTAATAAGAAACAGATTTTACTTAATAATATTTTAAATTTTCAAAAAGTATATC 11015
QY 147 AGATTATAGTAATCCATATGAAGCTGTGCAAGAGACATGAAAGCGAAGATTAACGG 206
DB 11014 TTATTAATCCGACGATTTTGCAACACGAGTGAAGAAAATAATCAAAATATATATATAGT 10955
QY 207 ATGAACCATTTACTAGCTTTGGCTGTATCAGACCAATTACTGAAATGACCTTGCTAG 266
DB 10954 AAATATTAATTAATTTGGATTTCTTTGATGTATTAATTAATAAAGAAATATTTATAGCA 10895
QY 267 CATGCCCTAAGTATTAAGAAAGTGAAGTGAAGAGATCTATATATTTTGGCTAACTTCTT 326
DB 10894 CAATACAGTAATTAATTAAGCTTATTAATAAATTAATAAGTTTATATATACAAA 10835
QY 327 TAGTTACTATTTGATGAT 344

Db 10834 AAGTATATATTTTCAT 10817

RESULT 11

ABL32893
ID ABL32893 standard; DNA, 10710 BP.

XX
AC ABL32893,
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 866.

XX
KW Human; immune system disease; cytosine methylation; antiaesthetic;
KW antileukemic; antineoplastic; cytosine methylation; antileukemic;
KW antineoplastic; anti-HIV; anticonvulsant; ophthalmological;
KW antineoplastic; antineoplastic; antidiabetic; antipsychotic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.

XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

XX
PS Claim 1; SEQ ID NO 866; 32pp + Sequence listing; German.

XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/intestinal bowel
CC diseases. The present sequence is a gene of the invention

XX
SQ Sequence 10710 BP; 3653 A; 81 C; 1963 G; 5013 T; 0 U; 0 Other;

Query Match 6.2%; Score 40.2; DB 6; Length 10710;
Best Local Similarity 50.3%; Pred. No. 2.4;
Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTAAGCTGCAAGCTTAA 63
DB 10207 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTAAGCTGCAAGCTTAA 10266

QY 64 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTAAGCTGCAAGCTTAA 123
DB 10267 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTAAGCTGCAAGCTTAA 10326

QY 124 TTAACTATATGTTGCTGCAATTAAGTATGATTAATCCATTAAGAGGCTTCAAGAA 183
DB 10327 TTAACTATATGTTGCTGCAATTAAGTATGATTAATCCATTAAGAGGCTTCAAGAA 10386

QY 184 ACATGAAGGCAAAAGAT 200

Db 10387 AGTTAAATATGATTAAT 10403

RESULT 12

ABK31213
ID ABK31213 standard; DNA, 19459 BP.

XX
AC ABK31213;
XX
DT 23-APR-2002 (first entry)
XX
DE Signal transduction associated gene modified complementary DNA #28.

XX
KW Human; signal transduction associated gene; cytosine methylation state;
KW CpG island; signal transduction associated disease; solid tumour; cancer;
KW antitumour; cytosine; mutant; ds.

XX
OS Homo sapiens.
XX
PN WO200200926-A2.
XX
PD 03-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-EP007472.
XX
PR 30-JUN-2000; 2000DE-01032529.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-147896/19.

PT Oligonucleotide for diagnosis and therapy of diseases associated with
PT signal transduction e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with signal transduction.

XX
PS Claim 1; SEQ ID NO 56; 24pp; English.

XX
CC The present invention relates to chemically modified DNA sequences of
CC signal transduction associated genes. The DNA sequences are chemically
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC the cytosine methylation state (CpG islands) of these genes, and a method
CC for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC genes associated with signal transduction. The genomic DNA can be
CC obtained from cells or cellular components which contain DNA, e.g. cell
CC lines, biopsies, blood, sputum, stool, urine, cerebral spinal fluid,
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC brain, heart, prostate, lung, breast or liver, histologic object slides,
CC and all their possible combinations. The sequences of the invention are
CC useful for the diagnosis and therapy of diseases associated with signal
CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC chemically pretreated genomic DNA sequences of different genes associated
CC with signal transduction, or their complementary sequences. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office

XX
SQ Sequence 19459 BP; 6064 A; 245 C; 3866 G; 9284 T; 0 U; 0 Other;

Query Match 6.2%; Score 40.2; DB 6; Length 19459;
Best Local Similarity 50.3%; Pred. No. 2.9;
Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTAAGCTGCAAGCTTAA 63
DB 4986 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTAAGCTGCAAGCTTAA 5045

QY 64 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTAAGCTGCAAGCTTAA 123

DB 5046 AGGTTAAAGCTAGATTTTAAATTTTAAAGAAATTTAGTATTTAT 5105
QY 124 TTTAACTATATGTGGTGCATATAGATTTATGATTAATCCATATGAAGGTTGCAGAGA 183
DB 5106 TTGAGTATATAGGTATGGGTAAAGATTTTATGTTTAAATTTAAAGTATGTTATATA 5165
QY 184 ACATGAAGGCAAAAGAT 200
DB 5166 AGTTAAATTTGATTAAT 5182

RESULT 13

ABL70528
ID ABL70528 standard; DNA; 19459 BP.

AC ABL70528;

XX 01-JUL-2002 (first entry)

DE Chemically treated cell signalling DNA sequence complementary to h209.

KW Cell signalling; cytosine methylation; cell signalling disease; cancer;
tumour; cytostatic; dr.

XX Unidentified.

OS WO200202807-A2.

XX 10-JAN-2002.

PF 29-JUN-2001; 2001WO-EP007471.

XX 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-154758/20.

PT Nucleic acid, useful for diagnosis and therapy of diseases associated
with cell signalling e.g. cancer, comprises chemically modified genomic
sequences of genes associated with cell signalling.

PS Claim 1; SEQ ID NO 418; 24pp + Sequence listing; English.

XX The invention relates to a nucleic acid comprising a sequence of at least
18 bases of a segment of chemically pretreated DNA of genes associated
with cell signalling. The activity of the modified sequences of the
invention may be described as cytostatic. The object of the invention is
to provide the chemically modified DNA of genes associated with cell
signalling, as well as oligonucleotides and/or PNA-oligonucleotides for
detecting cytosine methylations, as well as a method which is
particularly suitable for the diagnosis and/or therapy of genetic and
epigenetic parameters of genes associated with cell signalling. The
chemically modified DNA provided by the invention is useful for diagnosis
and therapy of diseases such as solid tumours and cancer. The sequences
given in records ABL70111-ABL70626 represent chemically pre-treated
genomic DNA's of genes associated with cell signalling. Note: The
sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
European Patent Office

XX Sequence 19459 BP; 6064 A; 245 C; 3866 G; 9284 T; 0 U; 0 Other;

QY Query Match 6.2%; Score 40.2; DB 6; Length 19459;

Best Local Similarity 50.3%; Pred. No. 2.9;

Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTTCAATTCGCTTCCTGTATGTTCTTATATTAATGATGCTGCAAAAGCTATA 63

DB 4986 AAAGTTGAATTCGATTTTTTTTTTATATTTATATATTAATTAAGATGATTA 5045
QY 64 AAGCTTGAATTCAGATATATATATTAACAAGTTAGTACAGATTTTGTACTCAAGTCT 123
DB 5046 AGGTTAAAGCTTAGATTTTAAATTTTAAAGAAATTTAGGTTATTTAT 5105
QY 124 TTTAACTATATGTGGTGCATATAGATTTATGATTAATCCATATGAAGGTTGCAGAGA 183
DB 5106 TTAGATATATAGGTATGGGTAAAGATTTTATGTTTAAATTTAAAGTATGTTATATA 5165
QY 184 ACATGAAGGCAAAAGAT 200
DB 5166 AGTTAAATTTGATTAAT 5182

RESULT 14

ABQ67006
ID ABQ67006 standard; DNA; 33053 BP.

XX ABQ67006;

XX 28-AUG-2002 (first entry)

DE Human angiogenesis associated polynucleotide SEQ ID NO 36.

KW Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcer;
macular degeneration; inflammatory bowel disease; Crohn's disease;
anti-rheumatic; anti-arthritis; antidiabetic; antiproliferative;
anti-arteriosclerotic; dr.

OS Homo sapiens.

XX WO200246454-A2.

XX 13-JUN-2002.

PF 06-DEC-2001; 2001WO-EP014320.

PR 06-DEC-2000; 2000DE-01061338.

PA (EPIG-) EPIGENOMICS AG.

PI Schacht O;

XX WPI; 2002-500450/53.

PT New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g. in
diagnosis or treatment of cancer.

PS Claim 1; SEQ ID NO 36; 41pp + Sequence listing; German.

XX The invention relates to a nucleic acid (I) comprising a segment of 18
bases of chemically pretreated DNA of angiogenesis-associated genes (II)
having sequences (ABQ66971-ABQ67178) or their complements. (I), also
related oligomers, are used to evaluate the methylation status and/or
CC single-nucleotide polymorphisms, in angiogenesis-related genes, for
diagnosis and treatment of eye diseases, proliferative retinopathy,
neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,
diabetic retinopathy, macular degeneration caused by neovascularisation,
psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
Crohn's disease. Note: The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 33053 BP; 10862 A; 283 C; 6271 G; 15637 T; 0 U; 0 Other;

QY Query Match 6.2%; Score 40.2; DB 6; Length 33053;

Best Local Similarity 50.3%; Pred. No. 3.4;

Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTTCAATTCGCTTCCTGTATGTTCTTATATTAATGATGCTGCAAAAGCTATA 63

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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:39:35 ; Search time 3703 Seconds
(without alignments)
8149.519 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645
Sequence: 1 GTCAGGTCGATTCGCTT.....TGTTCATGTCGAGGCTGC 645

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the change being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	96.9	973	10	CG154041 PUFZS22TB
2	603	93.5	819	9	CC642795 OGWDI19TV
3	517.2	80.2	994	10	CG154043 PUFZS22TD
4	383.8	59.5	872	8	CK607568 AVR1.29.B
5	382.4	59.3	432	10	CG042359 PUIU85TB
6	259	40.2	800	9	CC642785 OGMDI19TH
7	226.6	35.1	975	10	CG155200 PUKCN04TB
8	77	11.9	734	9	CC400812 PUBGX18TD
9	75.4	11.7	886	10	CG031509 PUJFL23TB
10	73.6	11.4	858	10	CG311059 OG5CY43TC
11	49.8	7.4	345	9	CC721634 OG2AD27TH
12	47.6	7.4	597	8	DN487904 R014B11.3
13	42.8	6.6	754	10	CL180658 104_390_1
14	41.8	6.5	375	3	BP526721 BP526721
15	41.8	6.5	684	9	CC950911 BO1BR08TF
16	41.6	6.4	650	6	CD293786 STRPUS36.
17	41.4	6.4	539	9	CC156622 1614e03.b
18	41.4	6.4	638	10	CG124220 PUFMB96TD
19	40.8	6.3	441	1	AL383889 MCBCL1E04
20	40.8	6.3	444	8	R39925 YF51e09.g1
21	40.6	6.3	347	9	BH473918 BOHNU33TR
22	40.6	6.3	773	9	B2236858 CH230-333

c	23	40.6	6.3	933	10	CNS00CFN	AL059220 Drosophila
c	24	40.6	6.3	1101	10	CNS0039G	AL063921 Drosophila
c	25	40.4	6.3	360	1	AL464043	AJ464043 Drosophila
c	26	40.4	6.3	1101	10	CNS00FMC	AL070972 Drosophila
c	27	40.4	6.3	1101	10	CNS0106X	AL098595 Drosophila
c	28	40.2	6.2	600	9	AQ395724	AQ395724 CTRBI-E1-
c	29	40.2	6.2	612	9	AQ390717	AQ390717 CTRBI-E1-
c	30	40.2	6.2	615	3	BJ315457	BJ315457 B3351457
c	31	40.2	6.2	658	3	BJ342361	BJ342361 B3342361
c	32	40.2	6.2	789	9	BZ606212	BZ606212 WHACB56TF
c	33	40.2	6.2	813	10	CZ703754	CZ703754 OC_Ba002
c	34	40.2	6.2	832	3	BM333797	BM333797 50072-2-1
c	35	40	6.2	747	10	AG605701	AG605701 Mus muscu
c	36	39.8	6.2	650	9	CC870062	CC870062 NDL.22D6
c	37	39.8	6.2	967	10	CNS00UTP	AL077063 Drosophila
c	38	39.6	6.1	604	10	CE428077	CE428077 E1gr-g88-
c	39	39.6	6.1	809	9	AZ670202	AZ670202 ENTJ167TF
c	40	39.6	6.1	877	9	AZ547430	AZ547430 ENTJCS5TR
c	41	39.6	6.1	975	5	BQ711132	BQ711132 AGENCOURT
c	42	39.6	6.1	985	10	CNS00CFN	AL058780 Drosophila
c	43	39.6	6.1	987	10	CNS014PQ	AL104456 Drosophila
c	44	39.4	6.1	491	10	CZ633677	CZ633677 OM_Ba017
c	45	39.4	6.1	1040	9	BZ463282	BZ463282 BONKO17TR

ALIGNMENTS

RESULT 1
CG154041 973 bp DNA linear GSS 21-AUG-2003
LOCUS PUFZS22TB_ZM_0.6_1.0_KB_Zea_mays genomic clone ZMBR0770C19,
DEFINITION genomic survey sequence.
ACCESSION CG154041 GI:34044842
VERSION CG154041.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 973)

REFERENCE
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFZS22TD
Contact: Cathy Whitelaw

TIGR
712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..973
Location/Qualifiers

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBR0770C19"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Query Match 96.9%; Score 625; DB 10; Length 973;
Best Local Similarity 99.1%; Pred. No. 5,1e-154;
Matches 639; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

1 GTCAGGTCGATTCGCTTCTGTATAGTTCTTATATTCATGCTGTGCAAGCT 60

Db 47 GTCAAGGTCGAATCTCTCTCTCTGTATGTTCTTATATACATCTCTGACAA-CT 105
QY 61 ATTAAGCTTGAATCTGAGATATAATATACAGTACTCTACAGAGTTTGTACTCAAG 120
Db 106 ATTAAGCTTGAATCTGAGATATAATATACAGTACTCTACAGAGTTTGTACTCAAG 165
QY 121 TCTTTTAACTATATGTTGTCATATAGATTATGATATCAATATGAGTGTGCAAG 180
Db 166 TCTTTTAACTATATGTTGTCATATAGATTATGATATCAATATGAGTGTGCAAG 225
QY 181 AGAATCATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTACAGCC 240
Db 226 CGAATATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTACAGCC 285
QY 241 AATTAATCTGAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGTGTGCAAG 300
Db 286 AATTAATCTGAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGTGTGCAAG 345
QY 301 ATCTATATTAATTTTGGCTAACTCTTTTATGTTACTATGATTAAGAAAGCTTACAT 360
Db 346 ATCTATATTAATTTTGGCTAACTCTTTTATGTTACTATGATTAAGAAAGCTTACAT 405
QY 361 GCCCATGCCAGCCCTTAATGTCGCGGTACATGATTAAGCAATATGATTAATTTACT 420
Db 406 GCCCATGCCAGCCCTTAATGTCGCGGTACATGATTAAGCAATATGATTAATTTACT 465
QY 421 CTATGTTCTCTCTTTTGTAGTGTGTATTAAGATGCTTTTGTGCGCACTGCAAG 480
Db 466 CTATGTTCTCTCTTTTGTAGTGTGTATTAAGATGCTTTTGTGCGCACTGCAAG 525
QY 481 ATGTTTACTTAATCTAGTGTGCAATGATTAAGAGTGTGCAAGTGTGCTGT 540
Db 526 ATGTTTACTTAATCTAGTGTGCAATGATTAAGAGTGTGCAAGTGTGCTGT 585
QY 541 AATCTACTGTACACACTACTGTGTGTGTCTTAACTCTTAATCTATTCACGTGCT 600
Db 586 AATCTACTGTACACACTACTGTGTGTGTCTTAACTCTTAATCTATTCACGTGCT 645
QY 601 AGTAATTAACCAATCTTAACAACACTGTGTATCATGTGTAGGGCTGC 645
Db 646 AGTAATTAACCAATCTTAACAACACTGTGTATCATGTGTAGGGCTGC 690

RESULT 2
CC642795 819 bp DNA linear GSS 19-JUN-2003
LOCUS OGM019TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZM5Bma0555C14,
DEFINITION CC642795 genomic survey sequence.
ACCESSION CC642795
VERSION CC642795.1 GI:32028363
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 819)
Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Konliffing,T.,
Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGM019TH
Contact: Cathy Whiteaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteaw@cigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers

source 1. .819
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM5Bma0555C14"
/note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

Query Match 93.5%; Score 603; DB 9; Length 819;
Best Local Similarity 98.8%; Pred. No. 3, 2e-148;
Matches 639; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY 1 GTCAAGGTCGAATCTCTCTCTCTGTATGTTCTTATATACATCTCTGACAA-CT 60
Db 158 GTCAAGGTCGAATCTCTCTCTCTGTATGTTCTTATATACATCTCTGACAA-CT 216
QY 61 ATTAAGCTTGAATCTGAGATATAATATACAGTACTCTACAGAGTTTGTACTCAAG 120
Db 217 ATTAAGCTTGAATCTGAGATATAATATACAGTACTCTACAGAGTTTGTACTCAAG 276
QY 121 TCTTTTAACTATATGTTGTCATATAGATTATGATATCAATATGAGTGTGCAAG 180
Db 277 TCTTTTAACTATATGTTGTCATATAGATTATGATATCAATATGAGTGTGCAAG 336
QY 181 AGAATCATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTACAGCC 240
Db 337 CGAATATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTACAGCC 396
QY 241 AATTAATCTGAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGTGTGCAAG 300
Db 397 AATTAATCTGAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGTGTGCAAG 456
QY 301 ATCTATATTAATTTTGGCTAACTCTTTTATGTTACTATGATTAAGAAAGCTTACAT 360
Db 457 ATCTATATTAATTTTGGCTAACTCTTTTATGTTACTATGATTAAGAAAGCTTACAT 516
QY 361 GCCCATGCCAGCCCTTAATGTCGCGGTACATGATTAAGCAATATGATTAATTTACT 420
Db 517 GCCCATGCCAGCCCTTAATGTCGCGGTACATGATTAAGCAATATGATTAATTTACT 576
QY 421 CTATGTTCTCTCTTTTGTAGTGTGTATTAAGATGCTTTTGTGCGCACTGCAAG 480
Db 577 CTATGTTCTCTCTTTTGTAGTGTGTATTAAGATGCTTTTGTGCGCACTGCAAG 636
QY 481 ATGTTTACTTAATCTAGTGTGCAATGATTAAGAGTGTGCAAGTGTGCTGT 540
Db 637 ATGTTTACTTAATCTAGTGTGCAATGATTAAGAGTGTGCAAGTGTGCTGT 696
QY 541 AATCTACTGTACACACTACTGTGTGTGTCTTAACTCTTAATCTATTCACGTGCT 599
Db 697 AATCTACTGTACACACTACTGTGTGTGTCTTAACTCTTAATCTATTCACGTGCT 756
QY 600 TAGTAATTAACCAATCTTAACAACACTGTGTATCATGTGTAGGGCTGC 645
Db 757 TAGTAATTAACCAATCTTAACAACACTGTGTATCATGTGTAGGGCTGC 803

RESULT 3
CG154043 994 bp DNA linear GSS 21-AUG-2003
LOCUS PUF2S22TD_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZM5Bma0770C19,
DEFINITION CG154043 genomic survey sequence.
ACCESSION CG154043
VERSION CG154043.1 GI:34044844
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE	1 (bases 1 to 994)
AUTHORS	Whiteleaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.
TITLE	Maize Genomics Consortium
JOURNAL	Unpublished (2003)
COMMENT	Other GS98: PUFZ522TB Contact: Cathy Whiteleaw TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whiteleaw@tigr.org Seq primer: TP Class: sheared ends.
FEATURES	Location/Qualifiers
source	1..994 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBTA0770C19" /clone_1lb="ZM.0.6.1.0 KB" /note="Vector: pCR4-TOPO. Site 1: EcoRI; 0.6-1.0 kb high COT selected genomic DNA library"
ORIGIN	
Query Match	80.2%; Score 517.2; DB 10; Length 994;
Best Local Similarity	98.5%; Pred. No. 1.5e-125;
Matches	522; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY	116 TCAAGCTCTTTAACTAATATGTTGGTCGAATTAAGATTATGAGTAATCCATATGAAGAGTTT 175
DB	994 TCAAGCTCTTTAACTAATATGTTGGTCGAATTAAGATTATGAGTAATCCATATGAAGAGTTGT 935
OY	176 GCAAGAGAACTGAAGGCAAGATAAAGCGATGAAGCAACCTTAAGCTTTGGCTGATC 235
DB	934 CAAGCGAATATGAAGGCAAGATAAAGCGATGAAGCAACCTTAAGCTTTGGCTGATTC 875
OY	236 AGACCAATTAAGTTGAATGCACTTGTGTAGCATGCTTAAGTATTTAGAAAGTAGCATG 295
DB	874 AGACCAATTAAGTTGAATGCACTTGTGTAGCATGCTTAAGTATTTAGAAAGTAGCATG 815
OY	296 GAGAAATCTAATATTTTGGCTAACTTTTGAATTAAGTATTAAGTATTAAGTATTAAGT 355
DB	814 GAGAAATCTAATATTTTGGCTAACTTTTGAATTAAGTATTAAGTATTAAGTATTAAGT 755
OY	356 CCATTTGCCCATGCCGACCTTAATGTCGGGAGCAATGATGAAGCAAGTATTAAT 415
DB	754 CCATTTGCCCATGCCGACCTTAATGTCGGGAGCAATGATGAAGCAAGTATTAAT 695
OY	416 TTAAGTATTAAGTCTTTTGGAGTCTGATTAAGTATGTCCTTTTGGAGCACTG 475
DB	694 TTAAGTATTAAGTCTTTTGGAGTCTGATTAAGTATGTCCTTTTGGAGCACTG 635
OY	476 AGAAGATTTAAGTCTTAAGTCTAGTGGCAATGATTAAGTCTAGTGGCAAGCATGTC 535
DB	634 AGAAGATTTAAGTCTTAAGTCTAGTGGCAATGATTAAGTCTAGTGGCAAGCATGTC 575
OY	536 TCTGTAATCTAAGTCTAGTGGCAATGATTAAGTCTAAGTCTAAGTCTAAGTCTAAGT 595
DB	574 TCTGTAATCTAAGTCTAGTGGCAATGATTAAGTCTAAGTCTAAGTCTAAGTCTAAGT 515
OY	596 TGGCTAGTAATTAAGCAATCATTTAACAACATGTTAAGTATTAAGTATTAAGTATTAAG 645
DB	514 TGGCTAGTAATTAAGCAATCATTTAACAACATGTTAAGTATTAAGTATTAAGTATTAAG 465
RESULT 4	
LOCUS	CK607568 872 bp mRNA linear EST 14-JAN-2005
DEFINITION	ANR1_29_B02.g1.A002 Anaerobic roots Sorghum bicolor cDNA clone
	ANR1_29_B02.A002.5', mRNA sequence.

ACCESSION	CX607568
VERSION	CX607568.1 GI:57806227
KEYWORDS	EST.
SOURCE	Sorghum bicolor (sorghum)
ORGANISM	Sorghum bicolor
TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Sorghum.
REFERENCE	1 (bases 1 to 872) Cordonier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R., Lim,S., Liang,C., Sun,F. and Pratt,L.H. A Sorghum EST database: anaerobic roots Unpublished (2005)
JOURNAL	Other_ESTS: ANR1_29_B02.bl_A002
COMMENT	Contact: Cordonier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel.: 706 542 1860 Fax: 706 583 0210 Email: mmprratt@uga.edu Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: Sugs (CTTCGCTCTAAAGCTCG).
FEATURES	Location/Qualifiers
SOURCE	1..872 /organism="Sorghum bicolor" /mol_type="mRNA" /culivar="Brx623" /db_xref="taxon:4558" /clone="ANR1_29_B02_A002" /lab_host="DH10B-T1 phage-resistant E. coli" /note="Organ: Root; Vector: pME188-FU3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA isolated from seedlings of sorghum Brx623 grown in hydroponic culture. At 8 days of age, medium was purged with nitrogen gas for 3 hr prior to stopping aeration. Roots were harvested after 3, 27, and 72 hr. Material from all time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME188-FU3 vector (5-prime DraIII site is CACTGTGTC, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."
ORIGIN	
Query Match	59.5%; Score 383.8; DB 8; Length 872;
Best Local Similarity	88.0%; Pred. No. 2.6e-90;
Matches 490; Conservative	0; Mismatches 52; Indels 15; Gaps 6;
Dy	5 AGTTCAATTGCCTTCCCTCGTATGTTCTTATATTACATGCTCGACAAGCTATAA 64
Dd	279 AAGTAAACCTGCTTCTCTCGTATGTTCT--TATTACATGCTCGACAGCTATGA 336
Dy	65 AGTTGATACTGCAGTATATATAACAAGTTAGCTACACAAGTTTGTAAGTCTT 124
Dd	337 TGCTTGATACGACGTCAATATATAACAAGTTAGCTACACAAGTTTGTAAGTCTT 396
Dy	125 TTAACTATATGTTGGTGCATTAAGAATTATAGTAATCATATGAAGGTTGCAAGGAA 184
Dd	397 TTAACATATATGTTGGTGCATTAAGAATTATAGTAATCATATGAAGGTTGCAAGGAA 456
Dy	185 CATGAAAAGCAAAGATAAACGATGAACCCATTACTAGCTTGGCTGTATCAGACATATA 244
Dd	457 CATGAAAAGCAAAGATAAACGATGAATTCATTACTAGCTTGGCTGTATTAACACATATA 516
Dy	245 ACTGAAAATGCACTTGGCTA--GCATGCCCTAAGTTTAGAAAAGGTAGCATGGAGAA 301

|||||
Db 517 ACTTG-ATTGCGCTTGCTACATGCGTGCCTAAATTAGAAAAGGTACATGAGAGAA 575
|||||
Qy 302 TCTATATATTTTGGCTAACTCTT-AGTTACATATGATGATGAGAAAGCCCTACCAT 360
|||||
Db 576 TCTATATATTTTGGCTAACTCTTCAAAATTACATGATGATGAGAAAGCCCTACCAT 635
|||||
Qy 361 GCCCATCCAGCCCTA---ATGTCCCGGTGACATGATGAGCCAGTACTATGATTAAT 416
|||||
Db 636 GCCATCCAGCATCTTATATGCTCGGTGACATGATGAGCCAGTACTATGATTAAT 695
|||||
Qy 417 TACTCTATTTGCTCTCTTTTGTAGTGTCTATTAAGATGTCCT---TTTGTAGCTAC 472
|||||
Db 696 AACCTATTTGCTCTCTTTTGTAGTGTCTATTAAGATGTCCTTTTCTTGTAGGCTAC 755
|||||
Qy 473 TCGAGAGATTTACTTAACTCTAGTGGCAATGATGAGCTCTGAGCAACGATG 532
|||||
Db 756 ACGAGAAAGTTTACTTAACTCTAGTGGCAATGATGAGCTCTCTGTATGATGTTG 815
|||||
Qy 533 TGCTCTGTAATCTACTG 549
|||||
Db 816 TCATCTCTTATTCATG 832

RESULT 5
CG042359 432 bp DNA linear GSS 19-AUG-2003
LOCUS CG042359
DEFINITION PULUB5TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMB7a0612P01,
genomic survey sequence.
ACCESSION CG042359
VERSION CG042359.1 GI:33914539
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Bkaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 432)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennezen,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PULUB5TD
Contact: Cathy WhiteLaw
TIGR

TITLE
JOURNAL
COMMENT
912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteLaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
Source
1..432
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB7a0612P01"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
cor selected genomic DNA library"

ORIGIN

Query Match 59.3%; Score 382.4; DB 10; Length 432;
Best Local Similarity 99.5%; Pred. No. 5.4e-90;
Matches 394; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 251 AATGCACTTGCTAGCATGCTAAGTATTAAGAAAGGTAGCAT-GGGAGATCTATATT 309
|||||
Db 7 AATGCACTTGCTAGCATGCTAAGTATTAAGAAAGGTAGCATGGGAGATCTATATT 66
|||||
Qy 310 ATTTGGCTAATCTTTAGTATGATGATGAGAAAGCCTACCATGCCCATGCC 369

|||||
Db 67 ATTTGGCTAATCTTTTGTATTAATGATGATGAGAAAGCCTACCATGCCATGCC 126
|||||
Qy 370 AGCCCTAATGTCCTGGGTGACATGATGAGCCAGTACTATGATTAATTTCTATTTGTC 429
|||||
Db 127 AGCCCTAATGTCCTGGGTGACATGATGAGCCAGTACTATGATTAATTTCTATTTGTC 186
|||||
Qy 430 TCTTTTGTAGTGTCTATTAAGATGTCCTTTTGTAGCCATCTGAGAGATGTTACT 489
|||||
Db 187 TCTTTTGTAGTGTCTATTAAGATGTCCTTTTGTAGCCATCTGAGAGATGTTACT 246
|||||
Qy 490 TAACTCTAGTGGCATGATGAGCTCTGACGCAACGATGCTCTGTAATCTACTG 549
|||||
Db 247 TAACTCTAGTGGCATGATGAGCTCTGACGCAACGATGCTCTGTAATCTACTG 306
|||||
Qy 550 TCAACGCTACTCTGTAGTGTGCTTAAACCTTAACTATTCACAGTGGCTAGTAATAC 609
|||||
Db 307 TCACCACTACCTGTATGATGCTTAACTCTTAACTATTCACAGTGGCTAGTAATAC 366
|||||
Qy 610 CAATCATTTTACAACACTGTATGATGAGGCTGC 645
|||||
Db 367 CAATCATTTTACAACACTGTATGATGAGGCTGC 402

RESULT 6
CC642785 800 bp DNA linear GSS 19-JUN-2003
LOCUS CC642785/c
DEFINITION OGMD19TH ZM 0.7_1.5_KB Zea mays genomic clone ZMMB4a0555C14,
genomic survey sequence.
ACCESSION CC642785
VERSION CC642785.1 GI:32028341
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Bkaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 800)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGMD19TV
Contact: Cathy WhiteLaw
TIGR

TITLE
JOURNAL
COMMENT
912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteLaw@tigr.org
Seq primer: TR
Class: methylation filtered.

FEATURES
Source
1..800
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB4a0555C14"
/clone_1lb="ZM_0.7_1.5_KB"
/note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 40.2%; Score 259; DB 9; Length 800;
Best Local Similarity 97.4%; Pred. No. 2.4e-57;
Matches 295; Conservative 0; Mismatches 5; Indels 3; Gaps 3;
Qy 346 AGAAGCTTACCAATTTG-CCCATGCCAGCCCTAATGTCCTGGTACATGATGAGCCAGTA 404
|||||
Db 800 AGAAGCTTACCAATTTGCTCCCATGCCAGCCCTAATGATCCCGTACATGATGAGCCAGTA 741
|||||
Qy 405 CTATGATTAATTAATCTATTTGTT-CTCCTTTTGTAGTGTGTATTAAGATGTCCTTTT 463

Db	740	CTAAGATTAAATTACTCTATTGTCTCTCTTTTGAAGTCTGTATGAATGTCCTTTT	681
Qy	464	TTGAGCCACTCGAAGAAGATGTTACTTAACCTCTAGTGGCAATGATTTGAGCTCTCAGTG	523
Db	680	TTGAGCCACTCGAAGAAGATGTTACTTAACCTCTAGTGGCAATGATTTGAGCTCTCAGTG	621
Qy	524	CAAGGCATGTGCTCTGTAAATCTACTGTGCAACCACTA-CTCTGTAGTGTGTGCTTAACTCT	582
Db	620	CAAGGCATGTGCTCTGTAAATCTACTGTGCAACCACTA-CTCTGTAGTGTGTGCTTAACTCT	561
Qy	583	AAACTATTCACGTCGGCTAGTAATTAACCAATCATTTACAAACACTTTACATGTGTAAGGC	642
Db	560	AAACTATTCACGTCGGCTAGTAATTAACCAATCATTTACAAACACTTTACATGTGTAAGGC	501
Qy	643	TGC 645	
Db	500	TGC 498	
RESULT 7			
LOCUS	CG155200/c		
DEFINITION	CG155200	975 bp	DNA
DEFINITION	PURKNO4TB ZM 0.6_1.0_KB zea	zeas	genomic clone ZMMBTa0788A08,
DEFINITION	genomic survey sequence.		
ACCESSION	CG155200		
VERSION	CG155200.1	GI:34046001	
KEYWORDS	GSF.		
SOURCE	zeas		
ORGANISM	zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 975)		
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Benick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Benneken,J.		
TITLE	Maize Genomes Consortium		
JOURNAL	Unpublished (2003)		
COMMENT	Other GSSs: PURKNO4TD		
	Contact: Cathy Whitelaw		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA		
	Tel: 301-838-5843		
	Fax: 301-838-0208		
	Email: whitelaw@tigr.org		
	Seq primer: 7R		
	Class: sheared ends.		
FEATURES	Location/Qualifiers		
source	1..975		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/strain="B73"		
	/db_xref="taxon:4577"		
	/clone="ZMMBTa0788A08"		
	/clone_1lb="ZM_0.6_1.0_KB"		
	/note="Vector: pCR4-TOPo; Site_1: EcoRI; 0.6-1.0 kb high		
	COT selected genomic DNA library"		
ORIGIN			
Query Match	35.1%	Score 226.6;	DB 10; Length 975;
Best Local Similarity	97.7%;	Pred. No. 8.9e-49;	
Matches 251; Conservative	0;	Mismatches 4;	Indels 2; Gaps 2;
Qy	1	GTCAAGTTCATTTCGCTGCTCTCTGTTATGTTCTTTATATTAACAGCTGACAAAGCT	60
Db	256	GTCAAGTTCATTTCGCTCTCTCTGTTATGTTCTTTATATTAACAGCTGACAA-CT	198
Qy	61	ATTAAGCTTGATATGCAATATATATATTAACAAGTTAGTACAAAGTTTGTACTTCAAG	120
Db	197	ATTAAGCTTGATATGCAAGTACATATATTAACAAGTTAGGACAAAGTTTGTACTTCAAG	138
Qy	121	TCTTTAACTATATGTTGGTGCAATTAAGATTATGATATCATATGAAGGTGGCAAG	180

Db	137	TCTTTTAACTCATTATGTTGGTCGACATAAGATTATGATTAATCCATATGAAGTGTTGCAG	78
Oy	181	AGAACATGAAGCGAAGAATPAACGATGAAACCATTACTAGCTTTGGCTGTATCA-G-C	239
Db	77	CGAATATGAAGCGAAGAATPAACGATGAAACCATTACTAGCTTTGGCTGTATCAGACC	18
Oy	240	CANAACTTGAAAATCA	256
Db	17	CNATTAAGTGAATGCA	1
<hr/>			
RESULT 8			
LOCUS	CC400812/c	734 bp	DNA linear GSS 19-MAY-2003
DEFINITION	PUEGX18TD ZM_0.6_1.0_KB Zea mays genomic clone ZMBRta249D12,		
ACCESSION	CC400812		
VERSION	CC400812.1		
KEYWORDS	GSS.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 734) Whitefaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennerzen,J.		
AUTHORS	Maize Genomics Consortium Unpublished (2003)		
TITLE	Contact: Cathy Whitefaw		
JOURNAL	tigr		
COMMENT	9712 Medical Center Drive, Rockville, MD 20850, USA Tel.: 301-838-5843 Fax: 301-838-0208 Email: whitefaw@tigr.org Seq primer: TP Class: sheared ends. Location/Qualifiers 1..734 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMBRta249D12" /clone_1kb="Zm_0.6_1.0_KB" /note="Vector: pCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high Cor selected genomic DNA library"		
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FEATURES			
source			
<hr/>			
ORIGIN			
Query Match	11.9%; Score 77;	DB 9;	Length 734;
Best Local Similarity	63.1%;	Pred. No. 2.8e-09;	
Matches 190;	Conservative 0;	Mismatches 70;	Indels 41; Gaps 3;
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Oy	280	TAGAAAAGTAGCATGGAGAAATCTAATATTTTGGCTAACTCTTTAGTTACTATTGA	339
Db	551	TAAACGACGCAACTGAAATTAATATGAAATGTTCTGGCTAACCTTCTTAATTACTATTGA	492
Oy	340	TTGATGAGAAAGCTTACCATTTGCCATGCGCACGCCCTAA-----TGTCCCGG	385
Db	491	TTGATGAGAAATCTTACCGTTTCCCATGCCCACGACACTACACTACTCTCTGTGCTCTGG	432
Oy	386	TGACATGATTGAGCGAGTACTATGATTAATTACTCTATTTGTTCTCTTTTTAGTGTCT	445
Db	431	TGACATGACGAGCGACATGACACTACATGATTAATGTTGCTCTCTTTTTGAGTGTCT	372
Oy	446	GTAATAGA-----TGTCCTTTTTTTGAGCCACTCGAGA	479
Db	371	ACTCCACAAGATGTCTCGGCTCTCTCTCTCTCTCTTTGTCGACCCACAGAGAA	312
Oy	480	GATG-TTACTTAATCTAGTGGCAATGATTTGAGGCTCTGATGCAACGATGTGCTCT	538

Db 311 GATGTTTACTTAAGTGCATGATGAAAGCTCTGTACTAGCGTGCCCT 252
Qy 539 G 539
Db 251 G 251

RESULT 9
CG031509 886 bp DNA 1linear GSS 19-AUG-2003
CG031509/c
LOCUS
DEFINITION
PUFRL23TB_ZM_0.6_1.0_KB Zea mays genomic clone ZMMB0656C22,
genomic survey sequence.
ACCESSION
CG031509
VERSION
CG031509.1 GI:33903665
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 886)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Benmetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFRL23TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
Source
1..886
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB0656C22"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN
Query Match 11.7%; Score 75.4; DB 10; Length 886;
Best Local Similarity 62.8%; Pred. No. 7.6e-09;
Matches 189; Conservative 0; Mismatches 71; Indels 41; Gaps 3;

Qy 280 TAGAAAGGTAGCATGGAGAAATATATTTGGCTAACTCTTAAGTACTATGA 339
Db 727 TAAACACGACACTTGAATATATGATGTTCTGGCTAACCTCTCTAGTACTATGA 668
Qy 340 TTGATGAAAGCCTACCATTTGCCATGCCAGCCCTAA-----TGTCCCG 385
Db 667 TTGATGAAATCTTACCGTTTCCATGCCACGACTACACTCTCTGTGCTCG 608
Qy 386 TGACATATGAGCGCACTACTATGATTAATTTACTTATGTTCTCTTTTGGAGTCT 445
Db 607 TGACATACCGAGCGCACTACTGATTAATGTTGCTCTCTTTTTCAGTGTCT 548
Qy 446 GTATTAAG-----TGTCTTTTGGAGCACTCGAGAA 479
Db 547 ACTCCAGAAATGCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 488
Qy 480 GATG-TTACTTAACTTAAGTGCAGATGATGAGCTCTCAAGTCAACGATGTGCTCT 538
Db 487 AATGTTTAACTTAAGTGCAGATGATGAGTGAAGCTCTCTCTCTCTCTCTCTCTCT 428
Qy 539 G 539

Db 427 G 427

RESULT 10
CG031059
LOCUS
DEFINITION
CG031059 858 bp DNA 1linear GSS 26-AUG-2003
CG031059/c
LOCUS
DEFINITION
O65CY43TC_ZM_0.7_1.5_KB Zea mays genomic clone ZMMB0834G13,
genomic survey sequence.
ACCESSION
CG031059
VERSION
CG031059.1 GI:34228219
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 858)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Maize Genomics Consortium
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.

FEATURES
Location/Qualifiers
Source
1..858
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB0834G13"
/note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
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Best Local Similarity 64.3%; Pred. No. 2.3e-08;
Matches 180; Conservative 0; Mismatches 59; Indels 41; Gaps 3;

Qy 301 ATCTAATATATTTTGGCTAACTCTTACTACTATGATGAAAGCCTACCAT 360
Db 5 ATATGAAATGTTCTGAGCTAACCTTCTCTAGTACTATGATGAAATCTACCGTT 64
Qy 361 GCCATGCGAGCCCTAA-----TGTCCCGTGAATGATGAGCCAGTACT 406
Db 65 TCCCATGCCACGACACTACACTCTCTGTCTCTGTGATGACGACGACAGTACA 124
Qy 407 ATGATTAATTAATTAATGTTCTCTTTTGGAGTGTATTAAG----- 453
Db 125 CTGACGATTAATTAATGTTGCTCTCTTTTTCAGAGTCACTCCAGAAATGTCCTG 184
Qy 454 -----TGTCTTTTGGAGCACTCGAGAGAGT-----TTACTTAATCTAGT 499
Db 185 CT 244
Qy 500 GCGCAATGATGAGCTCTCAAGTCAACGATGTGCTCTG 539
Db 245 GCACAAATGATTAAGCTCTCTGTACTAGCGTGTGCTCTG 284

RESULT 11
CC721634 345 bp DNA 1linear GSS 19-JUN-2003
CC721634/c
LOCUS
DEFINITION
O62AD27TH_ZM_0.7_1.5_KB Zea mays genomic clone ZMMB0741F06,
genomic survey sequence.
ACCESSION
CC721634

VERSION CC21634.1 GI:32126410
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Whiteley, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nuneberg, A., Robbins, D. and Lakey, N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: O62AD27TV
Contact: Cathy Whiteley
TIGR 9112 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteley@cigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. 345
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_1lb="ZM 0.7 1.5 KB"
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Query Match 7.7%; Score 49.8; DB 9; Length 345;
Best Local Similarity 71.0%; Pred. No. 0.038;
Matches 66; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 280 TAGAAAAGTACGATGGAGAACTATATTTTGGCTACCTTTTACTTACTATGA 339
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DB 246 TAAACACGACACTTGAATATATATGAAATGTTCTGCGCTAACCTTCTACTTACTATGA 305
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QY 340 TTGATGAGAAAGCTACCTATGCTCCATGCGCAGC 372
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DB 306 TTATATGAAATCTCTACCTTCCATGCCACC 338
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RESULT 12
DN487904 597 bp mRNA linear EST 10-MAR-2005
LOCUS DN487904.3pr Populus root cDNA library Populus tremula x Populus
DEFINITION tremuloides cDNA clone R014B11 3', mRNA sequence.
ACCESSION DN487904
VERSION DN487904
KEYWORDS
SOURCE
ORGANISM EST.
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
1 (bases 1 to 597)

REFERENCE
AUTHORS Sterry, P., Bhalerao, R.R., Unerberg, P., Segerman, B., Nilsson, P.,
Bruner, A.M., Chaboum, L., Lindvall, J.U., Tandir, K.,
Strasser, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P.,
Nilsson, O., Sandberg, G., Karlsson, J., Lundberg, J. and Jansson, S.
A Populus EST resource for plant functional genomics
Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
1535603
Other ESTs: R014B11, R014B11.5pr
Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
Umea University
901 87 Umea, Sweden

Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@plnphys.umu.se.
Location/Qualifiers
1. 597
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/clone_1lb="R014B11"
/issue_type="root"
/clone_1lb="Populus root cDNA library"

ORIGIN

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Best Local Similarity 51.1%; Pred. No. 0.16;
Matches 137; Conservative 0; Mismatches 129; Indels 2; Gaps 1;

QY 55 AAAGCTATAAGCTGTGATGATGATATATATACAAAT--TAGCTACACAAGTTTGT 112
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DB 425 AAAGCTATAAGCTGTGATGATGATATATATATACAAAT--TAGCTACACAAGTTTGT 366
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QY 113 ACTTCAAGCTTTTAACTATATATGTTGTCATTAAGATTATGATATTCATATGAAGT 172
|||
DB 365 AAAAATATTTTCAATATATGATGATGATATTAAGAAAAAATCAATTTAAAGAA 306
|||
QY 173 GTTGCAAGACATGAAAGCAAGATTAACGATGACCTTACTACTTGGCTGT 232
|||
DB 305 TTAGCCATTAACCTTAACAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 246
|||
QY 233 ATGAGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 292
|||
DB 245 TCAAGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 186
|||
QY 293 ATGAGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 320
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DB 185 TAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 158
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RESULT 13
CL180658 754 bp DNA linear GSS 06-JAN-2004
LOCUS CL180658.104 Sorghum bicolor genomic clone 10896176, genomic survey
DEFINITION (LibID: 104) Sorghum bicolor genomic clone 10896176, genomic survey
sequence.
ACCESSION CL180658
VERSION CL180658
KEYWORDS
SOURCE
ORGANISM Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 754)

REFERENCE
AUTHORS Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenemy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korf, I.P.,
Rabinowicz, P.D., Lakey, N., McComb, W.R., Beddell, J.A. and
Martensen, R.A.
Sorghum genome sequencing by methylation filtration
PLoS Biol. 3 (1), e13 (2005)
15660154

TITLE
JOURNAL
COMMENT
PUBMED
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriangenomics.com
Plate: 390 row: n column: 08
Seq primer: T3 Reverse
Class: methylation filtered
High quality sequence stop: 754.
Location/Qualifiers
1. 754

Best Local Similarity 50.2%; Pred. No. 5.5;
 Matches 103; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy	386	TGACATGATTGAGCCAGTACTATGATTAACTTACTCTATTGTTCTCCTTTTGAAGTCT	445
Db	138	TGACATCAATCTGCATTACTCCGGTATTCTATCTGGGTTTCTCCCTCGTTTCAC	197
Qy	446	GTAATAAGATGTCCTTTTGGAGCCACTCGAAGAGTGTACTTACTCTAGTGGCAA	505
Db	198	GTGAAAGCAGAGCTCGTGATGCCCCCAGAGTCTATCCCTGAAACTTCCCTCAGCAA	257
Qy	506	TGATTGAGCTCTCAGTGAAGCAGATGCTGTGTAATCTACTGTCAACCACTACTGTGTA	565
Db	258	GGATTAGATCTCTTAACATCATTTGAATTTGAGCTTTGAGTACCACAGAAATTACTAACCG	317
Qy	566	GTGTGTGCTTAAACTTAACATAATT	590
Db	318	CTGCCCCATTTGGCTCCCACTAATT	342

Search completed: February 12, 2006, 00:46:32
 Job time : 3707 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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; Sequence 9068, Application US/11098686

```
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9068
; LENGTH: 3222
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis

US-11-098-686-9068

Query Match          6.0%; Score 38.8; DB 11; Length 3222;
Best Local Similarity 43.9%; Pred. No. 0.65;
Matches 166; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 98 CTACACAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGGTGCATTAAGATTATAGT 157
DB 482 CCACGGAAGAAAGCGACATTAATGCTTAGAGTTCAAGGTAAACCTAAATAATAGGTAA 423
QY 158 AATCCATATGAAGGTGTGCAAGAAACATGAAGGCAAGATTAAGCATGAAACCAT 217
DB 422 TAGAGTCTTACTTGTGTTCAAGAGAGTGAAGAAATTCGAAACCTTTGACGGCAT 363
QY 218 ACTAGCTTGGCTGTATCAGACCAATTAAGTGAATGCACTTGCTAGCATGCGTAAT 277
DB 362 TCAATATTAAGTTTATTAAGTCTTCAACAAAGATCTGTGATTTATCAAGATCAATGA 303
QY 278 ATTAGAAAAGTAGCATGGAGAACTATATATTTTGGCTAACTCTTTAGTTACTATT 337
DB 302 AGTTTATAGCTACTGTAAGCAATATATGTTTACATACGCCATTAATGCTTCATGACAGT 243
QY 338 GATTGATGAGAAAGCCTACATTCATGCGACGCGCTTAATGTCGGTGCATGATGA 397
DB 242 CATGTATGAGAAACACGTGATCTTCAATATAAATAAATAGTGTGAGAAATGTTTGA 183
QY 398 GCCAGTACTATGATTAATTAATCTATGTTCTCTTTTGAAGTGTGATTAAGATGTC 457
DB 182 AATCTCTTCTGTACAAATCTGTCTATATACCAATATCAATGTTCTTTACGAATGTA 123
QY 458 CTTTTTGTGAGCCACTCG 475
DB 122 AGTTTGTGACACCATTG 105

RESULT 3
US-11-098-686-8739
; Sequence 8739, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8739
; LENGTH: 1457619
; TYPE: DNA
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; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739

Query Match          6.0%; Score 38.8; DB 11; Length 1457619;
Best Local Similarity 43.9%; Pred. No. 2.3;
Matches 166; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 98 CTACACAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGGTGCATTAAGATTATAGT 157
DB 210262 CCACGGAAGAAAGCGACATTAATGCTTAGAGTTCAAGGTAAACCTAAATAATAGGTAA 210321
QY 158 AATCCATATGAAGGTGTGCAAGAAACATGAAGGCAAGATTAAGCATGAAACCAT 217
DB 210322 TAGAGTCTTACTTGTGTTCAAGAGAGTGAAGAAATTCGAAACCTTTGACGGCAT 210381
QY 218 ACTAGCTTGGCTGTATCAGACCAATTAAGTGAATGCACTTGCTAGCATGCGTAAT 277
DB 210382 TCAATATTAATGTTTATTAAGTCTTCAACAAAGATCTGTGATTTATCAAGATCAATGA 210441
QY 278 ATTAGAAAAGTAGCATGGAGAACTATATATTTTGGCTAACTCTTTAGTTACTATT 337
DB 210442 AGTTTATAGCTACTGTAAGCAATATGTTTACATACGCCATTAATGCTTCATGACAGT 210501
QY 338 GATTGATGAGAAAGCCTACATTCATGCGACGCGCTTAATGTCGGTGCATGATGA 397
DB 210502 CATGTATGAGAAACACGTGATCTTCAATATAAATAAATAGTGTGAGAAATGTTTGA 210561
QY 398 GCCAGTACTATGATTAATTAATCTATGTTCTCTTTTGAAGTGTGATTAAGATGTC 457
DB 210562 AATCTCTTCTGTACAAATCTGTCTATATACCAATATCAATGTTCTTTACGAATGTA 210621
QY 458 CTTTTTGTGAGCCACTCG 475
DB 210622 AGTTTGTGACACCATTG 210639

RESULT 4
US-11-121-086-104
; Sequence 104, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 104
; LENGTH: 186442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-104

Query Match          6.0%; Score 38.4; DB 11; Length 186442;
Best Local Similarity 52.5%; Pred. No. 2.3;
Matches 84; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 260 GTGCTGACATGCTTAAGTATTAAGAAAGTAGCATGGAGAACTATATATTTTGGCTA 319
DB 133505 GTGTTACTATGCCCACTTAACAGATTAAGAAATGAGAACGACGTGAATTAAGTTA 133564
QY 320 ACTTCTTAAGTATCTATATGATGATGAGAAAGCTCAACTTGCCATGCGCAGCCCTAATG 379
DB 133565 TCTGTCTGTGTTACTCTGCTGCAAAATTAACACCCCAATCTTAAGAACTATGATTA 133624
QY 380 TCCCGGTGACATGATTAAGCCAGTACTATGATTAATTATC 419
DB 133625 TGCTATGTATTAATGATGAGTGAAGTTGAAACATGATCC 133664
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RESULT 5

US-10-623-155-88/C

/ Sequence 88, Application US/10623155
/ Publication No. US20050261166A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, Tonglong

/ APPLICANT: Peckham, David W.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Fanger, Gary R.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

/ FILE REFERENCE: 210121.455C20

/ CURRENT APPLICATION NUMBER: US/10/623.155

/ CURRENT FILING DATE: 2003-07-17

/ NUMBER OF SEQ ID NOS: 560

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 88

/ LENGTH: 1844

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-623-155-88

Query Match 5.8%; Score 37.2; DB 7; Length 1844;

Best Local Similarity 47.8%; Pred. No. 1.5;

Matches 108; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

/ 8 TTCAATTCCTGCTCTCTGTTATGTTCTTATATTAATCACTCTGACAAAGCTATTAAGC 67

/ 1599 TTTAATTTCAATTTCTCTCTCTATTAATTAACCTTTATTAAGATGTTTCCACTACAGT 1540

/ 68 TTGATATGAGATTAATTAATTAACAGTTACTACACAAAGTTTGTACTTCAAGCTTTTA 127

/ 1539 TTAACATATGAGCAAAATTTCCCAATTCACGTAATTTGGTTTAAACGGCAAGTTTAA 1480

/ 128 ACTAATATGTTGTCATATAGATTAATGATTAATCATATGATAGAGTGTGCAAGAACAT 187

/ 1479 ATGCTTTGAGATTCCTGAATACACCTTTGAACCTTCAATTAAGGTTATGTTTAATTT 1420

/ 188 GAAAGCAAAATTAACGATGAACCCATTACTAGCTTGGCTGTA 233

/ 1419 AACCTCATGATTAAGAGAGGACAGTTAGCTGATGCTCTTA 1374

RESULT 6

US-10-995-561-13483

/ Sequence 13483, Application US/10995561

/ Publication No. US20050272054A1

/ GENERAL INFORMATION:

/ APPLICANT: CARGILL, Michele et al.

/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

/ TITLE OF INVENTION: DETECTION AND USRS THEREOF

/ FILE REFERENCE: CLO01559

/ CURRENT APPLICATION NUMBER: US/10/995.561

/ CURRENT FILING DATE: 2004-11-24

/ NUMBER OF SEQ ID NOS: 85702

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 13483

/ LENGTH: 46215

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURES:

/ NAME/KEY: misc_feature

/ LOCATION: (1)...(46215)

/ OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10)

US-10-995-561-13483

Query Match 5.6%; Score 36.4; DB 7; Length 46215;

Best Local Similarity 52.7%; Pred. No. 5.5;

Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

/ 323 TCTTTAGTACTATGATGAGAAAGCTACATGCGCATGACCGCTTAATGCTC 382

/ 27870 TCTTTGTAAGTAATTCGAAATGAGAAAAATATTTTTCATTTTACCCACATCTTA 27929

/ 383 CGGTACATGATTTGAGCCAGTACTATGATTAATTTACTGATTTCTCTTTTGGAGT 442

/ 27930 CCATTTCTGCTGTTCTTCACTACTGTTGTAATGCTCCATCTGATGCTTTTCTT 27989

/ 443 GCTGTATTAAGATGCTCTTTTGTAGCCAC 472

/ 27990 TTCTTTTCTTTTCTTTTCTTTTGTAGACAC 28019

RESULT 7

US-11-117-187-209

/ Sequence 209, Application US/11117187

/ Publication No. US2005026560A1

/ GENERAL INFORMATION:

/ APPLICANT: PREUSS, DAPHNE

/ APPLICANT: COPEHNAVER, GREGORY

/ TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS

/ FILE REFERENCE: ARCD309US

/ CURRENT APPLICATION NUMBER: US/11/117.187

/ CURRENT FILING DATE: 2005-04-28

/ PRIOR APPLICATION NUMBER: US/09/531.120

/ PRIOR FILING DATE: 2000-03-17

/ PRIOR APPLICATION NUMBER: 60/125.219

/ PRIOR FILING DATE: 1999-03-18

/ NUMBER OF SEQ ID NOS: 212

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 209

/ LENGTH: 611587

/ TYPE: DNA

/ ORGANISM: Arabidopsis thaliana

US-11-117-187-209

Query Match 5.6%; Score 36.2; DB 11; Length 611587;

Best Local Similarity 54.0%; Pred. No. 12;

Matches 74; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

/ 82 TAATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAGTCTTTTAATTAATGTTGGT 141

/ 28263 TTAATTTAGAGTTAAAGTTCTAAAGTTATATATATATATATATATATATATTTTG 28322

/ 142 CATTAAGATTTATAGTAATTCATATGAAGTGTGCAAGAAACATGAAGCAAGATA 201

/ 28323 GTAAGATTTAAAGTTTATACATTTTATGTTTATTAACGAATTTCAAGATTTACAGG 28382

/ 202 AACGATGAACCATTA 218

/ 28383 AACGAATTAAGCAATA 28399

RESULT 8

US-11-136-527-941/C

/ Sequence 941, Application US/11136527

/ Publication No. US20050287570A1

/ GENERAL INFORMATION:

/ APPLICANT: Wyeth

/ APPLICANT: Mounts, William M

/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

/ FILE REFERENCE: 031896-04100 (AM101086)

/ CURRENT APPLICATION NUMBER: US/11/136.527

/ CURRENT FILING DATE: 2005-05-25

/ PRIOR APPLICATION NUMBER: US 60/574.294

/ PRIOR FILING DATE: 2005-05-26

/ NUMBER OF SEQ ID NOS: 362830

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 941

/ LENGTH: 566

/ TYPE: DNA

/ ORGANISM: Rattus norvegicus

US-11-136-527-941

	Query Match	5.4%	Score 34.8:	DB 11;	Length 566;
	Best Local Similarity	57.7%;	Pred. No. 5,		
	Matches	60;	Conservative	1;	Mismatches 43; Indels 0; Gaps 0;
Oy	397 AGCAGTCTATGATTAAATAACTTAATGTTCCTTTTGAGTGCCTAATAGAAGT	:			456
Dd	153 AGCCCTACTATGNAAAATCCCCCTCACTTGAATTGGCTGAATGAAGAAAAAAT		:		94
Oy	457 CTTTTTTTAGACCACTCGAGNAGATGTTTACTTAACCTAGTG				500
Dd	93 CTTTATTTGATATTTTCAGAGCATTTGCTCTAGATATG TG				50

```

RESULT 9
US-11-136-527-5037
: Sequence 5037, Application US/1136527
: Publication No. US20050287570A1
: GENERAL INFORMATION:
: APPLICANT: Wyeth
: APPLICANT: Wyeth
: TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
: FILE REFERENCE: 031896-04100 (AN101086)
: CURRENT APPLICATION NUMBER: US/11/136,527
: CURRENT FILING DATE: 2005-05-25
: PRIOR APPLICATION NUMBER: US 60/574,294
: PRIOR FILING DATE: 2005-05-26
: NUMBER OF SEQ. ID NOS: 362830
: SOFTWARE: Patentin version 3.2
: SEQ. ID NO 5037
: LENGTH: 566
: TYPE: DNA
: ORGANISM: Rattus norvegicus
US-11-136-527-5037

```

	Query Match	Similarity	Score	DB	length
Best Local	60	57.7%	34.8	11	566
Matches	60	Conservative	1	Mismatches	43
				Indels	0
				Gaps	0

	Query	DB
397	AGCCAGTACTATGATTAATTAATTAATCTATATGTCCTTTTGTGATGCTGTATAGATGT	456
414	AGCCCTACTATGTGAAATCCCCCTACTCTTAATTTGCTGAAATGAAGAAAATAAT	473
457	CCTTTTGTGAGCCACTCGAAGATGTTTACTTAATCTCTAGTG	500
474	CTTTATTTTGATATTTTTCAGAGCAATTTGCTCTAGATGTG	517

```

RESULT 10
US-10-903-375-34
; Sequence 34, Application US/10903375
; Publication No. US20060024794A1
GENERAL INFORMATION:
APPLICANT: LI, Shengwen
APPLICANT: AOKI, Kei Roger
TITLE OF INVENTION: Novel Methods for Production of D1-Chain Botulinum Toxin
FILE REFERENCE: ALLE0012-100 (ROI2003-147)
CURRENT APPLICATION NUMBER: US/10/903,375
CURRENT FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 2526
; TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleic acid sequence of HC
US-10-903-375-34

```

Query Match	5.4%	Score 34.8	DB 6	Length 2526
Best Local Similarity	47.3%	Pred. No. 7.2		
Matches 105; Conservative	0	Mismatches 117	Indels 0	Gaps 0
QY	84	ATATTAACAAGTTAGCTACACAAGTTTGTACTTCACAGTCTTTTAACTATATGTTGGTCA	143	

Db 1904 ATATTAATATATCTTTTAAATAGTCTTCATATACAAATGATGTAAAGATTATTTGGGGA 1963

Qy 144 ATTAAGATTATAGTATCATATGAGAGGTGTTCAGAGAACATGAAGCCAAAGATMA 203

Db 1964 ATGATCTTAGTATATATTAAGAAATATATATATGTAATATATGATTAATCTTAATAGATTA 2023

Qy 204 CGGATGAACCCATTACTAGCTTTGGCTGTATCAGACCATACTTGAATGCACTTGTGC 263

Db 2024 TGTATGCAATATGTAACAATTACTATTATTAATCAAGAGAGAAATATATATGATTTTATG 2083

Qy 264 TAGCATGCTTAAGTATTAGAAAAGATGACATGGAGAACTTA 305

Db 2084 AAGCATATTAATAATATATTAAGAAATATAGAGCAATATACA 2125

```

RESULT 11
US-11-121-086-72
: Sequence 72, Application US/11121086
: Publication No. US20050266459A1
: GENERAL INFORMATION:
: APPLICANT: POULSEN, TIM S.
: APPLICANT: NIELSEN, KIRSTEN V.
: TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
: FILE REFERENCE: 09138, 6000-00000
: CURRENT APPLICATION NUMBER: US/11/121, 086
: CURRENT FILING DATE: 2005-05-04
: PRIOR APPLICATION NUMBER: 60/567, 570
: PRIOR FILING DATE: 2004-05-04
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 72
: LENGTH: 162173
: TYPE: DNA
: ORGANISM: Homo sapiens
US-11-121-086-72

```

Query Match	5.4%	Score 34.8	DB 11	Length 162173
Best Local Similarity	54.8%	Pred. No. 20		
Matches	69	Conservative	0	Matches 57
			Indels	0
			Gaps	0
QY	520	AGTCAAGCAGCTGTCGTGTAATCTACGTGCACCACTACTGTAGTGTGCTTAAC	579	
DB	132077	ACTTGAGCCCAAGTGTCTTTGGATCCTACCTGGACCACTGCATCTCCAGCCTGGCAACA	132136	
QY	580	TCTAAACATATCCAGTGGCTGTATATACCATCATTTACAACACTGTTACATGTGTAG	639	
DB	132137	GCMAACCTCTGTCTCAAGAAAAAAGAAAGAAATACATATTTCCAGGGAAG	132196	

QY	640	GGCTGC	645
Db	132197	AGCAGC	132202

```

RESULT 12
US-11-091-018-1/c
/ Sequence 1, Application US/11091018
/ Publication No. US20050287551A1
/ GENERAL INFORMATION:
/ APPLICANT: GretaRedotlicr, Solveig
/ APPLICANT: Thorleifsson, Gudmar
/ APPLICANT: Gulcher, Jeffrey R.
/ TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
/ TITLE OF INVENTION: METHODS OF TREATMENT
/ FIDE REFERENCE: 2345.2010-016
/ CURRENT APPLICATION NUMBER: US/11/091.018
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: PCT/US03/29906
/ PRIOR FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: 10/255,120
/ PRIOR FILING DATE: 2002-09-25
/ PRIOR APPLICATION NUMBER: 10/419,723
/ PRIOR FILING DATE: 2003-04-18
/

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PRIOR APPLICATION NUMBER: 10/650,120
PRIOR FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: 10/067,514
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 09/811,352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PseSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1691140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1691140)
OTHER INFORMATION: nA,T,C or G
US-11-091-018-1

Query Match 5.4%; Score 34.6; DB 11; Length 1691140;
Best Local Similarity 52.4%; Pred. No. 39;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 8 TTCAATTCCTCTCTCTGTATGTTCTTATATTAACATGCTGACAAAGCTATAAGC 67
DB 1102792 TTAAATTCCTCTCTCTGATATTTATATTAAGAGCTGCTGACAAAGGCTGTCC 1102733
QY 68 TTGATCTGCAATTAATTAATTAACAGTACACAAAGTTTGTACTTCAAGCTTTTA 127
DB 1102732 ATAAATTTATTTGCAAAATTTCTGAGCATCTACTTCTGATTTTAAATCAATGTC 1102673
QY 128 ACTATATGTTGTGCAATTAAGATTA 152
DB 1102672 AGATATTTGGCTTAACATCAATCA 1102648

RESULT 13
US-10-750-185-29889/C
Sequence 29889, Application US/10750185
Publication NO. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29889
LENGTH: 601
TYPE: DNA
ORGANISM: Bovine 19866881745929
US-10-750-185-29889

Query Match 5.3%; Score 34.2; DB 7; Length 601;
Best Local Similarity 49.7%; Pred. No. 7.3;
Matches 87; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 115 TTCAATCTTTTACTATATGTTGTGCAATTAAGATTAATCCATATAGAGGT 174
DB 439 TTAAAGCTCTTTATTCCTTTGAAAGAGATTAGATTAGACTTAAGAGAGACTGTGAT 380
QY 175 TGCAGAGAAATGAAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTAT 234
DB 379 TCCATCAATTAAGAAATGTCATCAAGAGATGCTTTTAAAGCCTTTCTATTTGT 320

QY 235 CAGACCAATTAATTAAGATGCTGCTAGCATGCTTAATTAAGAAAGGT 289
DB 319 CTAAACATTAATTAAGAAAGATTAATTAATGCTTCCAGGTGTTATCAAGT 265

RESULT 14
US-10-750-623-29889/C
Sequence 29889, Application US/10750623
Publication NO. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29889
LENGTH: 601
TYPE: DNA
ORGANISM: Bovine 19866881745929
US-10-750-623-29889

Query Match 5.3%; Score 34.2; DB 7; Length 601;
Best Local Similarity 49.7%; Pred. No. 7.3;
Matches 87; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 115 TTCAATCTTTTACTATATGTTGTGCAATTAAGATTAATCCATATAGAGGT 174
DB 439 TTAAAGCTCTTTATTCCTTTGAAAGAGATTAGATTAGACTTAAGAGAGACTGTGAT 380
QY 175 TGCAGAGAAATGAAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTAT 234
DB 379 TCCATCAATTAAGAAATGTCATCAAGAGATGCTTTTAAAGCCTTTCTATTTGT 320
QY 235 CAGACCAATTAATTAAGATGCTGCTAGCATGCTTAATTAAGAAAGGT 289
DB 319 CTAAACATTAATTAAGAAAGATTAATTAATGCTTCCAGGTGTTATCAAGT 265

RESULT 15
US-10-750-185-62480
Sequence 62480, Application US/10750185
Publication NO. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62480
LENGTH: 3232
TYPE: DNA
ORGANISM: Bovine 19866880764359
US-10-750-185-62480

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Query Match      5.3%; Score 34.2; DB 7; Length 3232;
Best Local Similarity 52.4%; Pred. No. 11;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy      61  ATAAAGCTTGATCTGCACTATATATATACAGTTAGCTACACAGTTTGTACTTCAG 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2745 ATTATGCTGTACACCTGAACTAATATATATATATATCACTATGCTTCAATAAACA 2804

Qy      121  TCTTTTAACTATATGTGTGCAATAAGATTATGATATCCATATGAAGGTGTGCAAG 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2805 CTTTAAATATAAAAATGTGAAGAACAACATGAATAAAGCACTGGAATTAATATGCAA 2864

Qy      181  AGAACATGAAGGCAAGATAAA 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2865 AGAAAAAAAATCCAAAACAAAA 2887
  
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Search completed: February 12, 2006, 00:26:49
 Job time : 410 secs